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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 12:52:19 ; Search time 0.001 Seconds
(without alignments)
56.600 Million cell updates/sec

Title: US-10-619-220-65

Perfect score: 20
Sequence: 1 ccggaagaagaagtgcgtgga 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 131 seqs, 1415 residues

Total number of hits satisfying chosen parameters: 262

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 132 summaries

Database : usl0619220-65.rge.subdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	20	1 AR143179	ACCESSION:AR143179
C 2	20	100.0	20	1 BD249354	ACCESSION:BD249354
C 3	20	100.0	20	1 AR432273	ACCESSION:AR432273
C 4	12.4	62.0	15	1 I38970	ACCESSION:I38970
C 5	12.4	62.0	15	1 I38971	ACCESSION:I38971
C 6	12.4	62.0	15	1 AX635248	ACCESSION:AX635248
C 7	12.4	62.0	15	1 AX635250	ACCESSION:AX635250
C 8	11.4	57.0	13	1 AR175292	ACCESSION:AR175292
C 9	11.4	57.0	13	1 AR238749	ACCESSION:AR238749
C 10	10	50.0	11	1 Q835129	ACCESSION:Q835129
C 11	10	50.0	11	1 AX470593	ACCESSION:AX470593
C 12	10	50.0	11	1 AX624071	ACCESSION:AX624071
C 13	10	50.0	11	1 AX627751	ACCESSION:AX627751
C 14	10	50.0	11	1 AX629613	ACCESSION:AX629613
C 15	10	50.0	11	1 AX631492	ACCESSION:AX631492
C 16	10	50.0	12	1 AR030026	ACCESSION:AR030026
C 17	10	50.0	12	1 AR036346	ACCESSION:AR036346
C 18	10	50.0	12	1 AR036347	ACCESSION:AR036347
C 19	10	50.0	12	1 AR036365	ACCESSION:AR036365
C 20	10	50.0	12	1 AR036366	ACCESSION:AR036366
C 21	10	50.0	12	1 AR036368	ACCESSION:AR036368
C 22	10	50.0	12	1 I12563	ACCESSION:I12563
C 23	10	50.0	12	1 I12564	ACCESSION:I12564
C 24	10	50.0	12	1 I72094	ACCESSION:I72094
C 25	10	50.0	12	1 I72095	ACCESSION:I72095
C 26	10	50.0	12	1 I72113	ACCESSION:I72113
C 27	10	50.0	12	1 I72114	ACCESSION:I72114
C 28	10	50.0	12	1 I72116	ACCESSION:I72116
C 29	9.4	47.0	11	1 AR030110	ACCESSION:AR030110
C 30	9.4	47.0	11	1 Q832697	ACCESSION:Q832697
C 31	9.4	47.0	11	1 Q833073	ACCESSION:Q833073
C 32	9.4	47.0	11	1 Q833954	ACCESSION:Q833954
C 33	9.4	47.0	11	1 Q835815	ACCESSION:Q835815

34	9.4	47.0	11	1	Q837077	ACCESSION:Q837077
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36	9.4	47.0	11	1	AX470970	ACCESSION:AX470970
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62	8.4	42.0	10	1	E39661	ACCESSION:E39661
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106	8	40.0	10	1	AR261815	ACCESSION:AR261815

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c 120 8 40.0 10 1 AR489529
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129 8 40.0 10 1 AX153049
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131 8 40.0 10 1 BD063558
c 132 5.2 26.0 11 1 C0835815

ALIGNMENTS

RESULT 1
AR143179/c
LOCUS AR143179 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 73 from patent US 6204055.
ACCESSION AR143179
VERSION AR143179.1 GI:15104465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M. and Marcussen,E.G.
TITLE Antisense inhibition of Fas mediated signaling
JOURNAL Patent: US 6204055-A 73 20-MAR-2001;
FEATURES
LOCATION/Qualifiers
source 1..20
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Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
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BD249354/c
LOCUS BD249354 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of FAS mediated signaling.
ACCESSION BD249354
VERSION BD249354.1 GI:33059124
KEYWORDS JP 2002540812-A/69.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M. and Marcussen,E.G.
TITLE Antisense modulation of FAS mediated signaling
JOURNAL Patent: JP 2002540812-A 69 03-DEC-2002;

RESULT 3
AR432273/c
LOCUS AR432273 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 73 from patent US 6653133.
ACCESSION AR432273
VERSION AR432273.1 GI:40194546
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., Marcussen,E.G. and Wyatt,J.
TITLE Antisense modulation of Fas mediated signaling
JOURNAL Patent: US 6653133-A 73 25-NOV-2003;
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DEFINITION Sequence 8 from patent US 5616488.
ACCESSION I38970
VERSION I38970.1 GI:2083450
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 8 01-APR-1997;
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ACCESSION I38971
VERSION I38971.1 GI:2083451
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 9 01-APR-1997;
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RESULT 6
LOCUS AX635248/c 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 2387 from Patent EPI260586.
ACCESSION AX635248
VERSION AX635248.1 GI:28470862
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 2387 27-NOV-2002;
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Db 15 GGCAAGAAAGTGC 2

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ACCESSION AX635250
VERSION AX635250.1 GI:28470864
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 2389 27-NOV-2002;
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14 GGCAAGAAAGTGC 1

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DEFINITION Sequence 15 from patent US 6309823.
ACCESSION AR175292
VERSION AR175292.1 GI:17916591
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Cronin,M.T., Miyada,C.G., Hubbell,E.A., Chee,M., Fodor,S.P.A., Huang,X.C., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes for analyzing biotransformation genes and methods of using the same
JOURNAL Patent: US 6309823-A 15 30-OCT-2001;
FEATURES Location/Qualifiers
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LOCUS AR238749/c 13 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 15 from patent US 6468744.
ACCESSION AR238749
VERSION AR238749.1 GI:27283819
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Conrin,M.T., Sheldon,E.L., Miyada,C.G., Hubbell,E.A., Chee,M., Fodor,S.P.A., Huang,X.C., Lipshutz,R.J., Lobban,P.E. and Morris,M.S.
TITLE Analysis of genetic polymorphisms and gene copy number
JOURNAL Patent: US 6468744-A 15 22-OCT-2002;
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DEFINITION Sequence 187 from Patent WO2004059001.
ACCESSION CQ835129
VERSION CQ835129.1 GI:50834663
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O., Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 187 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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ACCESSION AX470593
VERSION AX470593.1 GI:22205718
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro

JOURNAL Patent: WO 02053773-A 170 11-JUL-2002;
HENKEL KGAA (DE)
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ACCESSION AX624071
VERSION AX624071.1 GI:28452012
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1112 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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ACCESSION AX627751
VERSION AX627751.1 GI:28455789
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4792 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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DEFINITION Sequence 6654 from Patent WO02053774.
ACCESSION AX629613
VERSION AX629613.1 GI:28457651
KEYWORDS Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6654 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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AX631492
LOCUS AX631492 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8534 from Patent WO02053774.
ACCESSION AX631492
VERSION AX631492.1 GI:28459558
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8534 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 100.0%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 16
AR030026
LOCUS AR030026 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 215 from patent US 5861244.
ACCESSION AR030026

VERSION AR030026.1 GI:5943240
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 215 19-JAN-1999;
FEATURES
source
1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 GGAAAGAAA 627
Db 3 GGAAAGAAA 12

RESULT 17
AR036346
LOCUS AR036346 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5872105.
ACCESSION AR036346
VERSION AR036346.1 GI:5953014
KEYWORDS Unknown.
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Single-stranded circular oligonucleotides useful for drug delivery
JOURNAL Patent: US 5872105-A 9 16-FEB-1999;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
Db 3 GAAAGAAAG 12

RESULT 18
AR036347/c
LOCUS AR036347 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5872105.
ACCESSION AR036347
VERSION AR036347.1 GI:5953015
KEYWORDS Unknown.
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Single-stranded circular oligonucleotides useful for drug delivery
JOURNAL Patent: US 5872105-A 10 16-FEB-1999;
FEATURES
source
1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 GGAAAGAAA 627
Db 1 GGAAAGAAA 10

RESULT 16
AR030026
LOCUS AR030026 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 215 from patent US 5861244.
ACCESSION AR030026

Qy 619 GAAAAGAAAG 628
Db 10 GAAAAGAAAG 1

RESULT 19
LOCUS AR036365
DEFINITION Sequence 28 from patent US 5872105.
ACCESSION AR036365
VERSION AR036365.1 GI:5953033
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Single-stranded circular oligonucleotides useful for drug delivery
JOURNAL Patent: US 5872105-A 28 16-FEB-1999;
FEATURES
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAAGAAAG 628
Db 1 GAAAAGAAAG 10

RESULT 20
LOCUS AR036366
DEFINITION Sequence 29 from patent US 5872105.
ACCESSION AR036366
VERSION AR036366.1 GI:5953034
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Single-stranded circular oligonucleotides useful for drug delivery
JOURNAL Patent: US 5872105-A 29 16-FEB-1999;
FEATURES
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAAGAAAG 628
Db 1 GAAAAGAAAG 10

RESULT 21
LOCUS AR036368/c
DEFINITION Sequence 31 from patent US 5872105.
ACCESSION AR036368
VERSION AR036368.1 GI:5953036
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)

Qy 619 GAAAAGAAAG 628
Db 1 GAAAAGAAAG 10

RESULT 22
LOCUS AR036367
DEFINITION Sequence 9 from patent US 5426180.
ACCESSION AR036367
VERSION AR036367.1 GI:909947
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Methods of making single-stranded circular oligonucleotides
JOURNAL Patent: US 5426180-A 9 20-JUN-1995;
FEATURES
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAAGAAAG 628
Db 12 GAAAAGAAAG 3

RESULT 23
LOCUS AR036368/c
DEFINITION Sequence 10 from patent US 5426180.
ACCESSION AR036368
VERSION AR036368.1 GI:909948
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Methods of making single-stranded circular oligonucleotides
JOURNAL Patent: US 5426180-A 10 20-JUN-1995;
FEATURES
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAAGAAAG 628
Db 3 GAAAAGAAAG 12

RESULT 24
LOCUS AR036369/c
DEFINITION Sequence 11 from patent US 5426180.
ACCESSION AR036369
VERSION AR036369.1 GI:909949
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Methods of making single-stranded circular oligonucleotides
JOURNAL Patent: US 5426180-A 11 20-JUN-1995;
FEATURES
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAAGAAAG 628
Db 10 GAAAAGAAAG 1

AUTHORS Kool,E.T.
TITLE Single-stranded circular oligonucleotides useful for drug delivery
JOURNAL Patent: US 5872105-A 31 16-FEB-1999;
FEATURES
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAAGAAAG 628
Db 12 GAAAAGAAAG 3

RESULT 25
LOCUS AR036370/c
DEFINITION Sequence 12 from patent US 5426180.
ACCESSION AR036370
VERSION AR036370.1 GI:909950
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Methods of making single-stranded circular oligonucleotides
JOURNAL Patent: US 5426180-A 12 20-JUN-1995;
FEATURES
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAAGAAAG 628
Db 3 GAAAAGAAAG 12

RESULT 26
LOCUS AR036371/c
DEFINITION Sequence 13 from patent US 5426180.
ACCESSION AR036371
VERSION AR036371.1 GI:909951
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Methods of making single-stranded circular oligonucleotides
JOURNAL Patent: US 5426180-A 13 20-JUN-1995;
FEATURES
source
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAAGAAAG 628
Db 10 GAAAAGAAAG 1

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAAGAAAG 628
Db 10 GAAAAGAAAG 1

RESULT 24
LOCUS I72094 12 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 9 from patent US 5683874.
ACCESSION I72094
VERSION I72094.1 GI:3008233
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Single-stranded circular oligonucleotides capable of forming a triplex with a target sequence
JOURNAL Patent: US 5683874-A 9 04-NOV-1997;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 619 GAAAGAAAG 628
|||||
Db 3 GAAAGAAAG 12
RESULT 25
LOCUS I72095 12 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 10 from patent US 5683874.
ACCESSION I72095
VERSION I72095.1 GI:3008234
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Single-stranded circular oligonucleotides capable of forming a triplex with a target sequence
JOURNAL Patent: US 5683874-A 10 04-NOV-1997;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 619 GAAAGAAAG 628
|||||
Db 3 GAAAGAAAG 12
RESULT 26
LOCUS I72113 12 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 28 from patent US 5683874.
ACCESSION I72113
VERSION I72113.1 GI:3008252
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Single-stranded circular oligonucleotides capable of forming a triplex with a target sequence
JOURNAL Patent: US 5683874-A 28 04-NOV-1997;

FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 619 GAAAGAAAG 628
|||||
Db 1 GAAAGAAAG 10
RESULT 27
LOCUS I72114 12 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 29 from patent US 5683874.
ACCESSION I72114
VERSION I72114.1 GI:3008253
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Single-stranded circular oligonucleotides capable of forming a triplex with a target sequence
JOURNAL Patent: US 5683874-A 29 04-NOV-1997;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 619 GAAAGAAAG 628
|||||
Db 1 GAAAGAAAG 10
RESULT 28
LOCUS I72116 12 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 31 from patent US 5683874.
ACCESSION I72116
VERSION I72116.1 GI:3008255
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Single-stranded circular oligonucleotides capable of forming a triplex with a target sequence
JOURNAL Patent: US 5683874-A 31 04-NOV-1997;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 619 GAAAGAAAG 628
|||||
Db 1 GAAAGAAAG 10
RESULT 29
LOCUS I72116/c 12 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 31 from patent US 5683874.
ACCESSION I72116
VERSION I72116.1 GI:3008255
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kool,E.T.
TITLE Single-stranded circular oligonucleotides capable of forming a triplex with a target sequence
JOURNAL Patent: US 5683874-A 31 04-NOV-1997;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 619 GAAAGAAAG 628
|||||
Db 12 GAAAGAAAG 3
RESULT 29

AR030110 LOCUS AR030110 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 299 from patent US 5861244.
ACCESSION AR030110
VERSION AR030110.1 GI:5943324
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Wang, C.-G. and Hepburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 299 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 618 GGAAGGAAAG 628
|||||
Db 1 GGAAGGAAAG 11

RESULT 30
LOCUS CQ832697 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 68 from Patent WO2004059002.
ACCESSION CQ832697
VERSION CQ832697.1 GI:50832304
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn, D., Schlotmann, K., Gassenmeier, T., Holtkoetter, O.,
Conradt, M. and Hofmann, K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 68 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGGAAAGT 629
|||||
Db 1 GAAAGGAAAGT 11

RESULT 31
LOCUS CQ833073/c 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 444 from Patent WO2004059002.
ACCESSION CQ833073
VERSION CQ833073.1 GI:50832680
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn, D., Schlotmann, K., Gassenmeier, T., Holtkoetter, O.,
Conradt, M. and Hofmann, K.

TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 444 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 622 AAGAAAGTGCT 632
|||||
Db 11 AAGAAAGTGCT 1

RESULT 32
LOCUS CQ833954 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1325 from Patent WO2004059002.
ACCESSION CQ833954
VERSION CQ833954.1 GI:50833561
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn, D., Schlotmann, K., Gassenmeier, T., Holtkoetter, O.,
Conradt, M. and Hofmann, K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 1325 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Tab. 2"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGGAAAGT 629
|||||
Db 1 GAAAGGAAAGT 11

RESULT 33
LOCUS CQ835815 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 873 from Patent WO2004059001.
ACCESSION CQ835815
VERSION CQ835815.1 GI:50835349
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn, D., Schlotmann, K., Gassenmeier, T., Holtkoetter, O.,
Conradt, M. and Hofmann, K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 873 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 32;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 622 AAGAAAGTCT 632
 Db 1 AAGAAAGTCT 11

RESULT 34
 CQ837077
 LOCUS CQ837077 11 bp DNA linear PAT 29-JUL-2004
 DEFINITION Sequence 2135 from Patent WO2004059001.
 ACCESSION CQ837077
 KEYWORDS CQ837077.1 GI:50836611
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
 Conradt,M. and Hofmann,K.
 TITLE Method for determining markers of human facial skin
 JOURNAL Patent: WO 2004059001-A 2135 15-JUL-2004;
 Henkel Kommanditgesellschaft auf Aktien (DE)
 FEATURES Location/Qualifiers
 source 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 32;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGAAAGT 629
 Db 1 GAAATAAAGT 11

RESULT 35
 AR241808
 LOCUS AR241808 11 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 96 from patent US 6472154.
 ACCESSION AR241808
 VERSION AR241808.1 GI:27287620
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 11)
 AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
 TITLE Polymorphic repeats in human genes
 JOURNAL Patent: US 6472154-A 96 29-OCT-2002;
 FEATURES Location/Qualifiers
 source 1..11
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 32;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 618 GGAAGGAAG 628
 Db 1 GGAAGGAAG 11

RESULT 36
 AX470970
 LOCUS AX470970 11 bp DNA linear PAT 09-AUG-2002

DEFINITION Sequence 547 from Patent WO2053773.
 ACCESSION AX470970 GI:22206095
 VERSION AX470970.1
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
 TITLE Method for determining skin stress or skin ageing in vitro
 JOURNAL Patent: WO 02053773-A 547 11-JUL-2002;
 HENKEL KGAA (DE)
 FEATURES Location/Qualifiers
 source 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 32;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGAAAGT 629
 Db 1 GAAATAAAGT 11

RESULT 37
 AX471396
 LOCUS AX471396 11 bp DNA linear PAT 09-AUG-2002
 DEFINITION Sequence 973 from Patent WO2053773.
 ACCESSION AX471396
 VERSION AX471396.1 GI:22206521
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens

REFERENCE 1
 AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
 TITLE Method for determining skin stress or skin ageing in vitro
 JOURNAL Patent: WO 02053773-A 973 11-JUL-2002;
 HENKEL KGAA (DE)
 FEATURES Location/Qualifiers
 source 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 32;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGAAAGT 629
 Db 1 GAAACCAAGT 11

RESULT 38
 AX622968
 LOCUS AX622968 11 bp DNA linear PAT 21-FEB-2003
 DEFINITION Sequence 9 from Patent WO02053774.
 ACCESSION AX622968
 VERSION AX622968.1 GI:28450909
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens

REFERENCE 1
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin

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JOURNAL Patent: WO 02053774-A 9 11-JUL-2002;
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGAAAGT 629
Db 1 GAAACCAAGT 11

RESULT 39
AX625367
LOCUS AX625367 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2408 from Patent WO02053774.
ACCESSION AX625367
VERSION AX625367.1 GI:28453308
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2408 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGAAAGT 629
Db 1 GAAACCAAGT 11

RESULT 40
AX627220/c
LOCUS AX627220 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4261 from Patent WO02053774.
ACCESSION AX627220
VERSION AX627220.1 GI:28455258
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4261 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGAAAGT 629
Db 1 GAAACCAAGT 11

RESULT 41
AX628179
LOCUS AX628179 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5220 from Patent WO02053774.
ACCESSION AX628179
VERSION AX628179.1 GI:28456217
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5220 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/organism="Homo sapiens"
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Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 622 AAGAAAGTGT 632
Db 1 AAGAAAGTCT 11

RESULT 42
AX630389
LOCUS AX630389 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7430 from Patent WO02053774.
ACCESSION AX630389
VERSION AX630389.1 GI:28458427
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7430 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 90.9%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGAAAGT 629
Db 1 GAAACCAAGT 11

RESULT 43
AR029878
LOCUS AR029878 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 67 from patent US 5861244.
ACCESSION AR029878

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VERSION AR029878.1 GI:5943092
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Wang, C.-G. and Hepburn, A.G.
 TITLE Genetic sequence assay using DNA triple strand formation
 JOURNAL Patent: US 5861244-A 67 19-JAN-1999;
 FEATURES Location/Qualifiers
 source 1..10
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 618 GGAAGAAGAA 626
 Db 2 GGAAGAAGAA 10
 RESULT 44
 AR241832 AR241832 10 bp DNA linear PAT 20-DEC-2002
 LOCUS Sequence 120 from patent US 6472154.
 DEFINITION AR241832
 ACCESSION AR241832
 VERSION AR241832.1 GI:27287644
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
 TITLE Polymorphic repeats in human genes
 JOURNAL Patent: US 6472154-A 120 29-OCT-2002;
 FEATURES Location/Qualifiers
 source 1..10
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 Query Match 45.0%; Score 9; DB 1; Length 10;
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 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 620 AAAAGAAG 628
 Db 2 AAAAGAAG 10
 RESULT 45
 AR561749 AR561749 10 bp DNA linear PAT 08-OCT-2004
 LOCUS Sequence 13 from patent US 6759195.
 DEFINITION AR561749
 ACCESSION AR561749
 VERSION AR561749.1 GI:53975400
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Bentley, W.E. and Gill, R.
 TITLE Method of differential display of prokaryotic messenger RNA by
 JOURNAL RT-PCR
 PATENT: US 6759195-A 13 06-JUL-2004;
 FEATURES Location/Qualifiers
 source 1..10
 /organism="unknown"
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 Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 33;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 626 AAGTGCTGG 634
 Db 2 AAGTGCTGG 10
 RESULT 46
 AX512724 AX512724 10 bp DNA linear PAT 03-OCT-2002
 LOCUS Sequence 51 from Patent WO02063044.
 DEFINITION AX512724
 ACCESSION AX512724
 VERSION AX512724.1 GI:23503942
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Anastasio, A.E., Chew, A., Denton, R.R., Nandabalan, K., Stephens, J.C. and Tirrell, C.
 TITLE Haplotypes of the ill5 gene
 JOURNAL Patent: WO 02063044-A 51 15-AUG-2002;
 Genaisance Pharmaceuticals, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..10
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 620 AAAAGAAG 628
 Db 1 AAAAGAAG 9
 RESULT 47
 AX512726 AX512726 10 bp DNA linear PAT 03-OCT-2002
 LOCUS Sequence 53 from Patent WO02063044.
 DEFINITION AX512726
 ACCESSION AX512726
 VERSION AX512726.1 GI:23503944
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Anastasio, A.E., Chew, A., Denton, R.R., Nandabalan, K., Stephens, J.C. and Tirrell, C.
 TITLE Haplotypes of the ill5 gene
 JOURNAL Patent: WO 02063044-A 53 15-AUG-2002;
 Genaisance Pharmaceuticals, Inc. (US)
 FEATURES Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 620 AAAAGAAG 628
 Db 2 AAAAGAAG 10
 RESULT 48
 AR029884

LOCUS AR029884 11 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 73 from patent US 5861244.
 ACCESSION AR029884
 VERSION AR029884.1 GI:5943098
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 11)
 AUTHORS Wang, C.-G. and Hepburn, A.G.
 TITLE Genetic sequence assay using DNA triple strand formation
 JOURNAL Patent: US 5861244-A 73 19-JAN-1999;
 FEATURES Location/Qualifiers
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 /mol_type="unassigned DNA"
 Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 619 GAAAGAGAAA 627
 Db |||||||
 2 GAAAGAGAAA 10
 RESULT 49
 CQ768938 Saitou, M. and Surani, A.
 LOCUS Genes
 DEFINITION Sequence 32 from Patent WO2004007723.
 ACCESSION CQ768938
 VERSION CQ768938.1 GI:45112300
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Saitou, M. and Surani, A.
 TITLE Genes
 JOURNAL Patent: WO 2004007723-A 32 22-JAN-2004;
 CAMBRIDGE UNIVERSITY TECHNICAL SERVICES LIMITED (GB)
 FEATURES Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
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 misc_feature 6 /note="n is a or g or c or t"
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 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 618 GGAAGAGAAA 627
 Db |||||||
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 RESULT 50
 CQ836350
 LOCUS
 DEFINITION Sequence 1408 from Patent WO2004059001.
 ACCESSION CQ836350
 VERSION CQ836350.1 GI:50835884
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Petersohn, D., Schlotmann, K., Gassenmeier, T., Holtkoetter, O.,
 Conrad, M. and Hofmann, K.

TITLE Method for determining markers of human facial skin
 JOURNAL Patent: WO 2004059001-A 1408 15-JUL-2004;
 Henkel Kommanditgesellschaft auf Aktien (DE)
 FEATURES Location/Qualifiers
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 Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 37;
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 QY 619 GAAAGAGAAA 627
 Db |||||||
 3 GAAAGAGAAA 11
 RESULT 51
 AX471219
 LOCUS
 DEFINITION Sequence 796 from Patent WO2053773.
 ACCESSION AX471219
 VERSION AX471219.1 GI:22206344
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Hofmann, K., Conrad, M. and Petersohn, D.
 TITLE Method for determining skin stress or skin ageing in vitro
 JOURNAL Patent: WO 02053773-A 796 11-JUL-2002;
 HENKEL KGAA (DE)
 FEATURES Location/Qualifiers
 source 1..11
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 Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 619 GAAAGAGAAA 627
 Db |||||||
 3 GAAAGAGAAA 11
 RESULT 52
 AX623377
 LOCUS
 DEFINITION Sequence 418 from Patent WO2053774.
 ACCESSION AX623377
 VERSION AX623377.1 GI:28451318
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Petersohn, D., Conrad, M. and Hofmann, K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 418 11-JUL-2002;
 Henkel Kommanditgesellschaft auf Aktien (DE)
 FEATURES Location/Qualifiers
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 /mol_type="unassigned DNA"
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 Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 37;
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Query Match          42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      618 GGAAGAAGAA 627
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Db      1 GGAAGAAGAA 10

RESULT 58
BD238688/c
LOCUS      BD238688
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD238688
VERSION    BD238688.1 GI:33048458
KEYWORDS   JP 2002534056-A/106.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 106 15-OCT-2002;
GENZYME    CORP

COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/106
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089977,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
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19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
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19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
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FEATURES
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Location/Qualifiers
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Query Match          42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      617 CGGAAGAGAA 626
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Db      1 CGGAAGAGAA 10

RESULT 60
BD239674/c
LOCUS      BD239674
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239674
VERSION    BD239674.1 GI:33049444
KEYWORDS   JP 2002534056-A/1092.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 1092 15-OCT-2002;
GENZYME    CORP

COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/647
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
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FEATURES
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Query Match          42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      620 AAAAGAAGT 629
|||||
Db      10 AAAAGAATGT 1

RESULT 59
BD239229
LOCUS      BD239229
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239229
VERSION    BD239229.1 GI:33048999
KEYWORDS   JP 2002534056-A/647.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 647 15-OCT-2002;
GENZYME    CORP

COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/647
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
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/organism='Homo sapiens (human)'.

FEATURES
source
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/mol_type='genomic DNA'
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Query Match          42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      620 AAAAGAAGT 629
|||||
Db      10 AAAAGAATGT 1

RESULT 59
BD239229
LOCUS      BD239229
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239229
VERSION    BD239229.1 GI:33048999
KEYWORDS   JP 2002534056-A/647.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 647 15-OCT-2002;
GENZYME    CORP

COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/647
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/1092
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
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19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
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08-DEC-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
CC Preparation and use of superior vaccines
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Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 623 AGAAGTGTCT 632
Db 10 AGAATGTGCT 1

RESULT 61
BD239990 10 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239990
VERSION BD239990.1 GI:33049760
KEYWORDS JP 2002534056-A/1408.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1408 15-OCT-2002;
COMMENT
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1408
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/090036,19-JUN-1998 US 60/089992 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR

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19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT Location/Qualifiers
/organism='Homo sapiens (human)'
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/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 621 AAAGAAAGTG 630
Db 1 AAGGAAAGTG 10

RESULT 62
E39661/c
LOCUS
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39661
VERSION E39661.1 GI:18621752
KEYWORDS JP 2000279181-A/194.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10)
AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE Genes with human dendritic cell expression
JOURNAL Patent: JP 2000279181-A 194 10-OCT-2000;
COMMENT SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN JP 2000279181-A/194
PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
PR
PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
C12N15/09,C07K14/475,C07K16/18,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
FT Location/Qualifiers
/organism='Homo sapiens (human)'
FEATURES
source
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/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 620 AAAAGAAAGT 629
Db 10 AAAAGAAAGT 1

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RESULT 63
AR303323
LOCUS AR303323 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 48 from patent US 6544736.
ACCESSION AR303323
VERSION AR303323.1 GI:31692099
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 48 08-APR-2003;
FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 624 GAAAGTCTG 633
Db 1 GAAAGAGCTG 10
RESULT 64
AR303346/c
LOCUS AR303346 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 71 from patent US 6544736.
ACCESSION AR303346
VERSION AR303346.1 GI:31692122
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 71 08-APR-2003;
FEATURES
source Location/Qualifiers
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Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 624 GAAAGTCTG 633
Db 1 GAAAGAGCTG 10
RESULT 65
AR336842
LOCUS AR336842 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 17 from patent US 6566130.
ACCESSION AR336842
VERSION AR336842.1 GI:33722692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
TITLE Androgen-regulated gene expressed in prostate tissue
JOURNAL Patent: US 6566130-A 17 20-MAY-2003;

FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 619 GAAAGAAAG 628
Db 1 GAAAGAGAGG 10
RESULT 66
AR364709
LOCUS AR364709 10 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 4 from patent US 5422251.
ACCESSION AR364709
VERSION AR364709.1 GI:34427644
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Fresco,J.R.
TITLE Triple-stranded nucleic acids
JOURNAL Patent: US 5422251-A 4 06-JUN-1995;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 619 GAAAGAAAG 628
Db 1 GGAAGAGAG 10
RESULT 67
AX152680
LOCUS AX152680 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 595 from Patent WO0138577.
ACCESSION AX152680
VERSION AX152680.1 GI:14534331
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 595 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 618 GGAAGAGAA 627
Db 1 GGAAGAGAAA 10

RESULT 68
AXI52681
LOCUS AXI52681 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 596 from Patent WO0138577.
ACCESSION AXI52681
VERSION AXI52681.1 GI:14534332
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptsomes
JOURNAL Patent: WO 0138577-A 596 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 618 GGAAAGAA 627
Db 1 GGAAAGAA 10
|||||
RESULT 69
AXI53193
LOCUS AXI53193 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1108 from Patent WO0138577.
ACCESSION AXI53193
VERSION AXI53193.1 GI:14534844
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptsomes
JOURNAL Patent: WO 0138577-A 1108 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 620 AAAAGAAAGT 629
Db 1 AAAAGAAACT 10
|||||
RESULT 70
BD007835/C
LOCUS BD007835 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007835
VERSION BD007835.1 GI:18636208
KEYWORDS JP 2001069993-A/111.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 111 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP.
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/111
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P39/00.
PC A61P31/00,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 620 AAAAGAAAGT 629
Db 10 AAAAGAAATGT 1
|||||
RESULT 71
BD083306
LOCUS BD083306 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083306
VERSION BD083306.1 GI:22628916
KEYWORDS JP 2001327293-A/227.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 227 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP.
COMMENT OS Homo sapiens (human)
PN JP 2001327293-A/227
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI
C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 620 AAAAGAAAGT 629
Db 1 AAAAGAAACT 10
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RESULT 72
BD083379/c
LOCUS      BD083379      10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION  BD083379
VERSION    BD083379.1  GI:22628989
KEYWORDS   JP 2001327293-A/300.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE     Human matured/activated dendritic cell expression genes
JOURNAL   Patent: JP 2001327293-A 300 27-NOV-2001;
          JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Homo sapiens (human)
           FN JP 2001327293-A/300
           PD 27-NOV-2001
           PF 22-MAY-2000 JP 2000150562
           PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI
             NAGAI
           PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
           CC
           FH Key      Location/Qualifiers.
FEATURES   source
            1..10      Location/Qualifiers
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy
Db      620 AAAAGAAAGT 629
        |||||
        10 AAAAGAATGT 1

RESULT 73
AR076623/c
LOCUS      AR076623      10 bp      DNA      linear      PAT 30-AUG-2000
DEFINITION Sequence 16 from patent US 5959094.
ACCESSION  AR076623
VERSION    AR076623.1  GI:10003369
KEYWORDS   AR076623.1  GI:10003369
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Wallach,D., Kuhnert,P., Ehrhardt,G. and Kemper,O.
TITLE     p75 TNF receptor promoters
JOURNAL   Patent: US 5959094-A 16 28-SEP-1999;
          Location/Qualifiers
FEATURES   source
            1..10      /organism="unknown"
                        /mol_type="unassigned DNA"
Query Match      41.0%; Score 8.2; DB 1; Length 10;
Best Local Similarity 70.0%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy
Db      619 GAAAGAAAG 628
        |||||
        10 GRAANGAAS 1

RESULT 74
AR076624
LOCUS      AR076624      10 bp      DNA      linear      PAT 30-AUG-2000
DEFINITION Sequence 17 from patent US 5959094.
ACCESSION  AR076624
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VERSION    AR076624.1  GI:10003370
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Wallach,D., Kuhnert,P., Ehrhardt,G. and Kemper,O.
TITLE     p75 TNF receptor promoters
JOURNAL   Patent: US 5959094-A 17 28-SEP-1999;
          Location/Qualifiers
FEATURES   source
            1..10      /organism="unknown"
                        /mol_type="unassigned DNA"
Query Match      41.0%; Score 8.2; DB 1; Length 10;
Best Local Similarity 70.0%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy
Db      619 GAAAGAAAG 628
        |||||
        1 GRAANGAAS 10

RESULT 75
E11042/c
LOCUS      E11042      8 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION Oligonucleotide as a probe for sequencing by hybridization.
ACCESSION  E11042
VERSION    E11042.1  GI:22024683
KEYWORDS   JP 1996070900-A/17.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 8)
AUTHORS   Fugono,N., Kurusu,Y., Terasawa,M. and Yugawa,H.
TITLE     ANALYSIS OF BASE SEQUENCE OF OLIGONUCLEOTIDE AND NUCLEIC ACID
JOURNAL   Patent: JP 1996070900-A 17 19-MAR-1996;
          MITSUBISHI CHEM CORP
COMMENT    OS None
           OC Artificial sequences.
           PN JP 1996070900-A/17
           PD 19-MAR-1996
           PF 13-FEB-1995 JP 1995024410
           PR 22-FEB-1994 JP 94P 24168, 29-JUN-1994 JP 94P 147291 PI
           FUGONO NOBUTAKE, KURUSU YASUO, TERASAWA MASATO, PI YUGAWA
           HIDEAKI
           PC C12Q1/68,C12N15/09;
           CC strandedness: Single;
           CC topology: Linear;
           FH Key      Location/Qualifiers
           FT source   1..8
           FT          /organism='Artificial sequences'.
           FT          Location/Qualifiers
           FT          1..8
           FT          /organism="unidentified"
           FT          /mol_type="genomic DNA"
           FT          /db_xref="taxon:32644"
Query Match      40.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
Db      618 GGAAGAAAG 625
        |||||
        8 GGAAGAAAG 1

RESULT 76
E12351
LOCUS      E12351      9 bp      DNA      linear      PAT 27-APR-1998
DEFINITION Oligonucleotide.
ACCESSION  E12351
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VERSION      E12352.1  GI:3251185
KEYWORDS     JP 1996319295-A/1.
SOURCE       unidentifed
ORGANISM     unclassified.
REFERENCE     1 (bases 1 to 9)
AUTHORS      Sugiyama,H., Hatano,T., Saito,R., Uchida,T., Matsuda,Y. and
              Uchida,K.
TITLE        NUCLEIC AID COMPOUND AND ITS SYNTHESIS
JOURNAL      Patent: JP 1996319295-A 1 03-DEC-1996;
              TOAGOSEI CO LTD
COMMENT      OS None
              OC Artificial sequences.
              PN JP 1996319295-A/1
              PD 03-DEC-1996
              PF 15-MAR-1996 JP 1996059574
              PR 22-MAR-1995 JP 95P 63188
              PI SUGIYAMA HIROSHI, HATANO TAKESHI, SAITO RETSU, PI UCHIDA
              TAKAYOSHI,
              PI MATSUDA YOKO, UCHIDA KIYOSHI
              PC C07J63/00,C07H21/00,C07J75/00;
              CC strandedness: Single;
              CC topology: Linear;
              FH Key
              FH Location/Qualifiers

FEATURES     source
              1..9
              /organism="Artificial sequences".
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"

Query Match  40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.le+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy           621 AAAGAAAG 628
Db           |||||||
            2 AAAGAAAG 2

RESULT 78
LOCUS       AR000251
DEFINITION Sequence 49 from patent US 5736336.
ACCESSION  AR000251
VERSION     AR000251.1  GI:3962782
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Buchardt,O. deceased, Buchardt,b.Dorte. representative, Egholm,M.,
              Nielsen,P.Eigil. and Berg,R.Henrik.
TITLE       Peptide nucleic acids having enhanced binding affinity, sequence
              specificity and solubility
JOURNAL     Patent: US 5736336-A 49 07-APR-1998;
FEATURES    source
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              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match  40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy           620 AAAGAAA 627
Db           |||||||
            2 AAAGAAA 9

RESULT 79
LOCUS       AR000253
DEFINITION Sequence 51 from patent US 5736336.
ACCESSION  AR000253
VERSION     AR000253.1  GI:3962784
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Buchardt,O. deceased, Buchardt,b.Dorte. representative, Egholm,M.,
              Nielsen,P.Eigil. and Berg,R.Henrik.
TITLE       Peptide nucleic acids having enhanced binding affinity, sequence
              specificity and solubility
JOURNAL     Patent: US 5736336-A 51 07-APR-1998;
FEATURES    source
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match  40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy           620 AAAGAAA 627
Db           |||||||
            2 AAAGAAA 9

RESULT 77
E12352/c
LOCUS       E12352
DEFINITION Oligonucleotide.
ACCESSION  E12352
VERSION     E12352.1  GI:3251186
KEYWORDS   JP 1996319295-A/2.
SOURCE     unidentifed
ORGANISM   unclassified.
REFERENCE   1 (bases 1 to 9)
AUTHORS     Sugiyama,H., Hatano,T., Saito,R., Uchida,T., Matsuda,Y. and
              Uchida,K.
TITLE        NUCLEIC AID COMPOUND AND ITS SYNTHESIS
JOURNAL      Patent: JP 1996319295-A 2 03-DEC-1996;
              TOAGOSEI CO LTD
COMMENT      OS None
              OC Artificial sequences.
              PN JP 1996319295-A/2
              PD 03-DEC-1996
              PF 15-MAR-1996 JP 1996059574
              PR 22-MAR-1995 JP 95P 63188
              PI SUGIYAMA HIROSHI, HATANO TAKESHI, SAITO RETSU, PI UCHIDA
              TAKAYOSHI,
              PI MATSUDA YOKO, UCHIDA KIYOSHI
              PC C07J63/00,C07H21/00,C07J75/00;
              CC strandedness: Single;
              CC topology: Linear;
              FH Key
              FH Location/Qualifiers

FEATURES     source
              1..9
              /organism="Artificial sequences".
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"

Query Match  40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.le+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy           621 AAAGAAAG 628
Db           |||||||
            1 AAAGAAAG 8

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FEATURES     source
              1..9
              /organism="Artificial sequences".
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"

Query Match  40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.le+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy           621 AAAGAAAG 628
Db           |||||||
            9 AAAGAAAG 2

RESULT 78
LOCUS       AR000251
DEFINITION Sequence 49 from patent US 5736336.
ACCESSION  AR000251
VERSION     AR000251.1  GI:3962782
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Buchardt,O. deceased, Buchardt,b.Dorte. representative, Egholm,M.,
              Nielsen,P.Eigil. and Berg,R.Henrik.
TITLE       Peptide nucleic acids having enhanced binding affinity, sequence
              specificity and solubility
JOURNAL     Patent: US 5736336-A 49 07-APR-1998;
FEATURES    source
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match  40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy           620 AAAGAAA 627
Db           |||||||
            2 AAAGAAA 9

RESULT 79
LOCUS       AR000253
DEFINITION Sequence 51 from patent US 5736336.
ACCESSION  AR000253
VERSION     AR000253.1  GI:3962784
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Buchardt,O. deceased, Buchardt,b.Dorte. representative, Egholm,M.,
              Nielsen,P.Eigil. and Berg,R.Henrik.
TITLE       Peptide nucleic acids having enhanced binding affinity, sequence
              specificity and solubility
JOURNAL     Patent: US 5736336-A 51 07-APR-1998;
FEATURES    source
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Query Match  40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy           620 AAAGAAA 627
Db           |||||||
            2 AAAGAAA 9

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Db 1 AAAAGAAA 8

RESULT 80
LOCUS AR087158 10 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 4 from patent US 5986053.
ACCESSION AR087158
VERSION AR087158.1 GI:10013922
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Mollegaard,N.E.
TITLE Peptide nucleic acids complexes of two peptide nucleic acid strands and one nucleic acid strand
JOURNAL Patent: US 5986053-A 4 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 81
LOCUS AR087171 10 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 43 from patent US 5986053.
ACCESSION AR087171
VERSION AR087171.1 GI:10013934
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Mollegaard,N.E.
TITLE Peptide nucleic acids complexes of two peptide nucleic acid strands and one nucleic acid strand
JOURNAL Patent: US 5986053-A 43 16-NOV-1999;
FEATURES Location/Qualifiers
source 1..10
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/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 82
LOCUS AR145664 10 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6218108.
ACCESSION AR145664
VERSION AR145664.1 GI:15108853
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Mollegaard,N.E.
TITLE Peptide nucleic acids complexes of two peptide nucleic acid strands and one nucleic acid strand
JOURNAL Patent: US 6218108-A 1 17-APR-2001;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 83
LOCUS AR150606 10 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 20 from patent US 6228982.
ACCESSION AR150606
VERSION AR150606.1 GI:15115197
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Norden,B., Wittung,P., Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.
TITLE Double-stranded peptide nucleic acids
JOURNAL Patent: US 6228982-A 20 08-MAY-2001;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 84
LOCUS AR150608 10 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 22 from patent US 6228982.
ACCESSION AR150608
VERSION AR150608.1 GI:15115199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Norden,B., Wittung,P., Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.
TITLE Double-stranded peptide nucleic acids
JOURNAL Patent: US 6228982-A 22 08-MAY-2001;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 85
LOCUS AR150609 10 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 23 from patent US 6228982.
ACCESSION AR150609
VERSION AR150609.1 GI:15115200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Norden,B., Wittung,P., Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.
TITLE Double-stranded peptide nucleic acids
JOURNAL Patent: US 6228982-A 23 08-MAY-2001;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

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Db      1 AAAAGAAA 8
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RESULT 85
LOCUS   BD144711
DEFINITION Peptide nucleic acid having elevated binding affinity, sequence
ACCESSION BD144711
VERSION   BD144711.1 GI:27850469
KEYWORDS JP 2002105059-A/49.
SOURCE   unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Nielsen,P.A., Einhorn,M. and Berg,R.H.
TITLE    Peptide nucleic acid having elevated binding affinity, sequence
JOURNAL  Patent: JP 2002105059-A 49 10-APR-2002;
COMMENT  DORTE BUCHARDT,PETER A NIELSEN,MICHAEL EINHORN,ROLF HO BERG
PN JP 2002105059-A/49
PD 10-APR-2002
PF 23-JUL-2001 JP 2001222248
PR 24-JUL-1996 US 08/685484,24-JUL-1996 US 08/686116 PR
24-JUL-1996 US 08/686114,24-JUL-1996 US 08/686113 PR
29-MAY-1997 US 60/051002
PI OLE BUCHARDT,PETER A NIELSEN,MICHAEL EINHORN,ROLF HO BERG PC
C07D233/64,C12N15/09,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Peptide nucleic acid having elevated binding affinity, CC
sequence
CC specificity and solubility
FH Key Location/Qualifiers
FT source 1..10
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Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 1 AAAAGAAA 8
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RESULT 87
LOCUS   BD161405/c
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161405
VERSION   BD161405.1 GI:27867163
KEYWORDS JP 2002186482-A/227.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE    Nagai,S., Matsushima,K. and Hashimoto,S.
JOURNAL  Human activated Th1 and Th2 cell expression genes
Patent: JP 2002186482-A 227 02-JUL-2002;
COMMENT  JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/227
PD 02-JUL-2002
PF 19-DEC-2000 JP 200385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
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FT source 1..10
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 616 CCGGAAAA 623
Db 9 CCGGAAAA 2
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RESULT 88
LOCUS   BD166477
DEFINITION linear
PAT 17-JAN-2003

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PF 23-JUL-2001 JP 2001222248
PR 24-JUL-1996 US 08/685484,24-JUL-1996 US 08/686116 PR
24-JUL-1996 US 08/686114,24-JUL-1996 US 08/686113 PR
29-MAY-1997 US 60/051002
PI OLE BUCHARDT,PETER A NIELSEN,MICHAEL EINHORN,ROLF HO BERG PC
C07D233/64,C12N15/09,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Peptide nucleic acid having elevated binding affinity, CC
sequence
CC specificity and solubility
FH Key Location/Qualifiers
FT source 1..10
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Location/Qualifiers
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Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 1 AAAAGAAA 8
|||||

RESULT 87
LOCUS   BD161405/c
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161405
VERSION   BD161405.1 GI:27867163
KEYWORDS JP 2002186482-A/227.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE    Nagai,S., Matsushima,K. and Hashimoto,S.
JOURNAL  Human activated Th1 and Th2 cell expression genes
Patent: JP 2002186482-A 227 02-JUL-2002;
COMMENT  JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/227
PD 02-JUL-2002
PF 19-DEC-2000 JP 200385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
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Location/Qualifiers
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Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 616 CCGGAAAA 623
Db 9 CCGGAAAA 2
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RESULT 88
LOCUS   BD166477
DEFINITION linear
PAT 17-JAN-2003

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DEFINITION Human liver disease-expressing genes.
ACCESSION BD166477
VERSION BD166477.1 GI:27872289
KEYWORDS JP 2002209591-A/22.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 22 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/22
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02.
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
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Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 622 AAGAAAGT 629
Db 3 AAGAAAGT 10
RESULT 89
LOCUS BD167010 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167010
VERSION BD167010.1 GI:27872822
KEYWORDS JP 2002209591-A/555.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 555 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/555
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02.
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
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Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 622 AAGAAAGT 629
Db 3 AAGAAAGT 10
RESULT 90
LOCUS BD239174 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239174
VERSION BD239174.1 GI:33048944
KEYWORDS JP 2002534056-A/592.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 592 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/592
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
GOIN37/00,
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
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Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 618 GGAAGAAGA 625
Db 2 GGAAGAAGA 9
RESULT 91
LOCUS BD239216 10 bp DNA linear PAT 17-JUL-2003

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DEFINITION      Preparation and use of superior vaccines.
ACCESSION       BD239216
VERSION         BD239216.1  GI:33048986
KEYWORDS        JP 2002534056-A/634.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 10)
AUTHORS         Roberts,B.L. and Shankara,S.
TITLE           Preparation and use of superior vaccines
JOURNAL         Patent: JP 2002534056-A 634 15-OCT-2002;
                GENZYME CORP
COMMENT         OS Homo sapiens (human)
                PN JP 2002534056-A/634
                PD 15-OCT-2002
                PF 18-JUN-1999 JP 2000554749
                PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
                PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
                PR 19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
                PR 19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
                PR 19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
                PR 19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
                PR 19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
                PR 19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
                PR 19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
                PR 19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
                PR 19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
                PR 19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
                PR 19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
                PR 19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
                08-DEC-1998 US 60/111715
                PI BRUCE L ROBERTS,SRINIVAS SHANKARA
                PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
                C12N1/19,
                PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
                G01N37/00,
                PC C12N15/00,C12N5/00,C12N15/00
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                FT source 1..10
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  ACCESSION       E36057
  VERSION         E36057.1  GI:13022459
  KEYWORDS        JP 1999236396-A/2.
  SOURCE          unidentified
  ORGANISM        unclassified.
  1 (bases 1 to 10)
  AUTHORS         Morugado,N.A.
  TITLE           Higher-order structure and binding of peptide nucleic acid
  JOURNAL         Patent: JP 1999236396-A 2 31-AUG-1999;
                ISIS PHARMACEUTICALS INC,BUCHARDT DORUTE,EGUHORUMU MICHAEL, IELSEN

Query Match     40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 623 AGAAGTG 630
Db 1 AGAAGTG 8
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RESULT 92
E36057
LOCUS            Higher-order structure and binding of peptide nucleic acid.
DEFINITION
ACCESSION       E36057
VERSION         E36057.1  GI:13022459
KEYWORDS        JP 1999236396-A/2.
SOURCE          unidentified
ORGANISM        unclassified.
1 (bases 1 to 10)
AUTHORS         Morugado,N.A.
TITLE           Higher-order structure and binding of peptide nucleic acid
JOURNAL         Patent: JP 1999236396-A 2 31-AUG-1999;
                ISIS PHARMACEUTICALS INC,BUCHARDT DORUTE,EGUHORUMU MICHAEL, IELSEN

PATER A, BERGH RORUFU HO
OS Unidentified
PN JP 1999236396-A/2
PD 31-AUG-1999
PF 14-OCT-1998 JP 1998291590
PR 02-JUL-1993 US 088658
PI BUSHATO ORE,EGUHORUMU MICHAEL,NIELSEN PATER A,BERG RORUFU HO,
PI EKKA DAVID JAY,MORUGADO NILUS A
PC C07H21/04,A61K31/00,A61K31/00,A61K31/00,A61K31/70,A61K48/00,
PC C07H21/02,
PC C12N15/09,C12O1/68,C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
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Query Match     40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 2 AAAAGAAA 9
|||||

RESULT 93
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LOCUS            Higher-order structure and binding of peptide nucleic acid.
DEFINITION
ACCESSION       E36070
VERSION         E36070.1  GI:13022472
KEYWORDS        JP 1999236396-A/15.
SOURCE          unidentified
ORGANISM        unclassified.
1 (bases 1 to 10)
AUTHORS         Bushato,O., Eguhorumu,M., Nielsen,P.A., Berg,R.H., Ekka,D.J. and
                Morugado,N.A.
TITLE           Higher-order structure and binding of peptide nucleic acid
JOURNAL         Patent: JP 1999236396-A 15 31-AUG-1999;
                ISIS PHARMACEUTICALS INC,BUCHARDT DORUTE,EGUHORUMU MICHAEL, IELSEN

PATER A, BERGH RORUFU HO
OS Unidentified
PN JP 1999236396-A/15
PD 31-AUG-1999
PF 14-OCT-1998 JP 1998291590
PR 02-JUL-1993 US 088658
PI BUSHATO ORE,EGUHORUMU MICHAEL,NIELSEN PATER A,BERG RORUFU HO,
PI EKKA DAVID JAY,MORUGADO NILUS A
PC C07H21/04,A61K31/00,A61K31/00,A61K31/00,A61K31/70,A61K48/00,
PC C07H21/02,
PC C12N15/09,C12O1/68,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
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FT source 1..10
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Query Match     40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PATER A, BERGH RORUFU HO
OS Unidentified
PN JP 1999236396-A/2
PD 31-AUG-1999
PF 14-OCT-1998 JP 1998291590
PR 02-JUL-1993 US 088658
PI BUSHATO ORE,EGUHORUMU MICHAEL,NIELSEN PATER A,BERG RORUFU HO,
PI EKKA DAVID JAY,MORUGADO NILUS A
PC C07H21/04,A61K31/00,A61K31/00,A61K31/00,A61K31/70,A61K48/00,
PC C07H21/02,
PC C12N15/09,C12O1/68,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Unidentified'.

FEATURES
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  /organism='unidentified'
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Query Match     40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 94
LOCUS 149613 10 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 4 from patent US 5641625.
ACCESSION I49613
VERSION I49613.1 GI:2471833
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Mollegaard,N.E.
TITLE Cleaving double-stranded DNA with peptide nucleic acids
JOURNAL Patent: US 5641625-A 4 24-JUN-1997;
FEATURES
source Location/Qualifiers
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/organism="unknown"
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Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 95
LOCUS 149626 10 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 43 from patent US 5641625.
ACCESSION I49626
VERSION I49626.1 GI:2471846
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Mollegaard,N.E.
TITLE Cleaving double-stranded DNA with peptide nucleic acids
JOURNAL Patent: US 5641625-A 43 24-JUN-1997;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 96
LOCUS 149613 10 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 49 from patent US 5719262.
ACCESSION I83584
VERSION I83584.1 GI:3407114
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O. deceased, Buchardt,b.Dorte. legalrepresentative, Egholm,M., Nielsen,P.Eigil. and Berg,R.Henrik.
TITLE Peptide nucleic acids having enhanced binding affinity, sequence
JOURNAL Patent: US 5719262-A 49 17-FEB-1998;
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source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O. deceased, Buchardt,b.Dorte. representative, Egholm,M., Nielsen,P.Eigil. and Berg,R.Henrik.
TITLE Peptide nucleic acids having enhanced binding affinity, sequence
JOURNAL Patent: US 5719262-A 49 03-FEB-1998;
FEATURES
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/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 97
LOCUS 183586 10 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 51 from patent US 5714331.
ACCESSION I83586
VERSION I83586.1 GI:3407116
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O. deceased, Buchardt,b.Dorte. representative, Egholm,M., Nielsen,P.Eigil. and Berg,R.Henrik.
TITLE Peptide nucleic acids having enhanced binding affinity, sequence
JOURNAL Patent: US 5714331-A 51 03-FEB-1998;
FEATURES
source Location/Qualifiers
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Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 98
LOCUS 188952 10 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 49 from patent US 5719262.
ACCESSION I88952
VERSION I88952.1 GI:3408892
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O. deceased, Buchardt,b.Dorte. legalrepresentative, Egholm,M., Nielsen,P.Eigil. and Berg,R.Henrik.
TITLE Peptide nucleic acids having amino acid side chains
JOURNAL Patent: US 5719262-A 49 17-FEB-1998;
FEATURES
source Location/Qualifiers
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/organism="unknown"
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Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 99
LOCUS 188954
DEFINITION Sequence 51 from patent US 5719262. linear PAT 10-AUG-1998
ACCESSION I88954
VERSION I88954.1 GI:3408894
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O. deceased, Buchardt,b.Dorte. legalrepresentative,
Egholm,M., Nielsen,P.Egil. and Berg,R.Henrik.
TITLE Peptide nucleic acids having amino acid side chains
JOURNAL Patent: US 5719262-A 51 17-FEB-1998;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Qy 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 100
LOCUS AR200459
DEFINITION Sequence 2 from patent US 6357163. linear PAT 20-APR-2002
ACCESSION AR200459
VERSION AR200459.1 GI:20251347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Use of nucleic acid analogues in diagnostics and analytical procedures
JOURNAL Patent: US 6357163-A 2 19-MAR-2002;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Qy 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 101
LOCUS AR200462
DEFINITION Sequence 5 from patent US 6357163. linear PAT 20-APR-2002
ACCESSION AR200462
VERSION AR200462.1 GI:20251350
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Use of nucleic acid analogues in diagnostics and analytical procedures
JOURNAL Patent: US 6357163-A 5 19-MAR-2002;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Qy 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 102
LOCUS AR200471/c
DEFINITION Sequence 14 from patent US 6357163. linear PAT 20-APR-2002
ACCESSION AR200471
VERSION AR200471.1 GI:20251359
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Use of nucleic acid analogues in diagnostics and analytical procedures
JOURNAL Patent: US 6357163-A 14 19-MAR-2002;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Qy 620 AAAAGAAA 627
Db 9 AAAAGAAA 2

RESULT 103
LOCUS AR200473/c
DEFINITION Sequence 16 from patent US 6357163. linear PAT 20-APR-2002
ACCESSION AR200473
VERSION AR200473.1 GI:20251361
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Use of nucleic acid analogues in diagnostics and analytical procedures
JOURNAL Patent: US 6357163-A 16 19-MAR-2002;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
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Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Qy 620 AAAAGAAA 627
Db 10 AAAAGAAA 3

RESULT 104
LOCUS AR241792 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 80 from patent US 6472154.
ACCESSION AR241792
VERSION AR241792.1 GI:27287604
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 80 29-OCT-2002;
FEATURES
source Location/Qualifiers
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/organism="unknown"
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Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 621 AAAGAAAG 628
Db 9 AAAGAAAG 2

RESULT 105
LOCUS AR241854 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 142 from patent US 6472154.
ACCESSION AR241854
VERSION AR241854.1 GI:27287666
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 142 29-OCT-2002;
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 621 AAAGAAAG 628
Db 3 AAAGAAAG 10

RESULT 106
LOCUS AR261815 10 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 241 from patent US 6322995.
ACCESSION AR261815
VERSION AR261815.1 GI:28072955
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hohmann,H.-P., Humbelin,M., van Loon,A. and Schurter,W.

Qy 621 AAAGAAAG 628
Db 3 AAAGAAAG 10

RESULT 107
LOCUS AR303415 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 140 from patent US 6544736.
ACCESSION AR303415
VERSION AR303415.1 GI:31692191
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watabiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 140 08-APR-2003;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 617 CGGAAAAG 624
Db 1 CGGAAAAG 8

RESULT 108
LOCUS AR303483/c 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 208 from patent US 6544736.
ACCESSION AR303483
VERSION AR303483.1 GI:31692259
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watabiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 208 08-APR-2003;
FEATURES
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/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 617 CGGAAAAG 624
Db 1 CGGAAAAG 8

RESULT 109
LOCUS AR303483 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 208 from patent US 6544736.
ACCESSION AR303483
VERSION AR303483.1 GI:31692259
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watabiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 208 08-APR-2003;
FEATURES
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/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 617 CGGAAAAG 624
Db 10 CGGAAAAG 3

RESULT 109
AR371271
LOCUS AR371271 10 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 8 from patent US 6395474.
ACCESSION AR371271
VERSION AR371271.1 GI:34608203
JOURNAL
FEATURES
source
ORGANISM Unknown.
SOURCE Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 8 28-MAY-2002;
LOCATION/Qualifiers
FEATURES
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 110
AR371272
LOCUS AR371272 10 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 9 from patent US 6395474.
ACCESSION AR371272
VERSION AR371272.1 GI:34608204
JOURNAL
FEATURES
source
ORGANISM Unknown.
SOURCE Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 9 28-MAY-2002;
LOCATION/Qualifiers
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/mol_type="genomic DNA"
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 111
AR371273
LOCUS AR371273 10 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 10 from patent US 6395474.
ACCESSION AR371273
VERSION AR371273.1 GI:34608205
JOURNAL
FEATURES
source
ORGANISM Unknown.
SOURCE Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 10 28-MAY-2002;
LOCATION/Qualifiers
FEATURES
source

/organism="unknown"
/mol_type="genomic DNA"
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 112
AR371275/c
LOCUS AR371275 10 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 12 from patent US 6395474.
ACCESSION AR371275
VERSION AR371275.1 GI:34608207
JOURNAL
FEATURES
source
ORGANISM Unknown.
SOURCE Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 12 28-MAY-2002;
LOCATION/Qualifiers
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/mol_type="genomic DNA"
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 620 AAAAGAAA 627
Db 9 AAAAGAAA 2

RESULT 113
AR371277/c
LOCUS AR371277 10 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 14 from patent US 6395474.
ACCESSION AR371277
VERSION AR371277.1 GI:34608209
JOURNAL
FEATURES
source
ORGANISM Unknown.
SOURCE Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 14 28-MAY-2002;
LOCATION/Qualifiers
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/mol_type="genomic DNA"
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 620 AAAAGAAA 627
Db 10 AAAAGAAA 3

RESULT 114
AR392569
LOCUS AR392569 10 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 56 from patent US 6613873.
ACCESSION AR392569

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VERSION AR392569.1 GI:40116633
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids having 2,6-diaminopurine nucleobases
JOURNAL Patent: US 6613873-A 56 02-SEP-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 620 AAAAGAAA 627
Db 2 AAAAGAAA 9
RESULT 115
AR392571
LOCUS AR392571 10 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 58 from patent US 6613873.
ACCESSION AR392571
VERSION AR392571.1 GI:40116635
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids having 2,6-diaminopurine nucleobases
JOURNAL Patent: US 6613873-A 58 02-SEP-2003;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 620 AAAAGAAA 627
Db 1 AAAAGAAA 8
RESULT 116
AR489492
LOCUS AR489492 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 8 from patent US 6710163.
ACCESSION AR489492
VERSION AR489492.1 GI:47256517
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acid synthons
JOURNAL Patent: US 6710163-A 8 23-MAR-2004;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 620 AAAAGAAA 627
Db 1 AAAAGAAA 8
RESULT 117
AR489494
LOCUS AR489494 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 10 from patent US 6710163.
ACCESSION AR489494
VERSION AR489494.1 GI:47256519
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acid synthons
JOURNAL Patent: US 6710163-A 10 23-MAR-2004;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 620 AAAAGAAA 627
Db 2 AAAAGAAA 9
RESULT 118
AR489496/c
LOCUS AR489496/c 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 12 from patent US 6710163.
ACCESSION AR489496
VERSION AR489496.1 GI:47256521
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acid synthons
JOURNAL Patent: US 6710163-A 12 23-MAR-2004;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 620 AAAAGAAA 627
Db 9 AAAAGAAA 2
RESULT 119
AR489498/c
LOCUS AR489498 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 14 from patent US 6710163.
ACCESSION AR489498
VERSION AR489498.1 GI:47256523
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
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AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acid synthons
JOURNAL Patent: US 6710163-A 14 23-MAR-2004;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
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Db 10 AAAAGAAA 3

RESULT 120
AR489529/c LOCUS 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 46 from patent US 6710163.
ACCESSION AR489529
VERSION AR489529.1 GI:47256554
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acid synthons
JOURNAL Patent: US 6710163-A 14 23-MAR-2004;
FEATURES Location/Qualifiers
source
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Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
| | | | |
Db 10 AAAAGAAA 3

RESULT 121
AR489578 LOCUS 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 49 from patent US 6710164.
ACCESSION AR489578
VERSION AR489578.1 GI:47256603
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nielsen,P.E., Egholm,M., Berg,R.H., Buchardt,O. and Buchardt,D.
TITLE Peptide nucleic acids having enhanced binding affinity, sequence specificity and solubility
JOURNAL Patent: US 6710164-A 49 23-MAR-2004;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
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Db 2 AAAAGAAA 9

RESULT 122
AR489580 LOCUS 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 51 from patent US 6710164.
ACCESSION AR489580
VERSION AR489580.1 GI:47256605
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nielsen,P.E., Egholm,M., Berg,R.H., Buchardt,O. and Buchardt,D.
TITLE Peptide nucleic acids having enhanced binding affinity, sequence specificity and solubility
JOURNAL Patent: US 6710164-A 51 23-MAR-2004;
FEATURES Location/Qualifiers
source
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
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Db 1 AAAAGAAA 8

RESULT 123
AR491103 LOCUS 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 8 from patent US 6713602.
ACCESSION AR491103
VERSION AR491103.1 GI:47258963
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Buchardt,D., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Synthetic procedures for peptide nucleic acids
JOURNAL Patent: US 6713602-A 8 30-MAR-2004;
FEATURES Location/Qualifiers
source
1. .10
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/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
| | | | |
Db 2 AAAAGAAA 9

RESULT 124
AR491105 LOCUS 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 10 from patent US 6713602.
ACCESSION AR491105
VERSION AR491105.1 GI:47258965
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Buchardt,O., Buchardt,D., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Synthetic procedures for peptide nucleic acids
JOURNAL Patent: US 6713602-A 10 30-MAR-2004;
FEATURES Location/Qualifiers

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source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 1 AAAAGAAA 8
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RESULT 125
AR491107/c AR491107 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 12 from patent US 6713602.
ACCESSION AR491107
VERSION AR491107.1 GI:47258967
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Buchardt, D., Egholm, M., Nielsen, P.E. and Berg, R.H.
TITLE Synthetic procedures for peptide nucleic acids
JOURNAL Patent: US 6713602-A 12 30-MAR-2004;
FEATURES
source 1..10
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/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 9 AAAAGAAA 2
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RESULT 126
AR491109/c AR491109 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 14 from patent US 6713602.
ACCESSION AR491109
VERSION AR491109.1 GI:47258969
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Buchardt, D., Egholm, M., Nielsen, P.E. and Berg, R.H.
TITLE Synthetic procedures for peptide nucleic acids
JOURNAL Patent: US 6713602-A 14 30-MAR-2004;
FEATURES
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAA 627
Db 10 AAAAGAAA 3
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RESULT 127
AX152470 AX152470 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 385 from Patent WO0138577.
LOCUS
Qy 620 AAAAGAAA 627
Db 10 AAAAGAAA 3
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ACCESSION AX152470
VERSION AX152470.1 GI:14534121
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcripts
JOURNAL Patent: WO 0138577-A 385 31-MAY-2001;
FEATURES
source 1..10
Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 628 GTGCTGGA 635
Db 2 GTGCTGGA 9
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RESULT 128
AX152632 AX152632 10 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 547 from Patent WO0138577.
ACCESSION AX152632
VERSION AX152632.1 GI:14534283
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcripts
JOURNAL Patent: WO 0138577-A 547 31-MAY-2001;
FEATURES
source 1..10
Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 628 GTGCTGGA 635
Db 1 GTGCTGGA 8
|||||

RESULT 129
AX153049 AX153049 10 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 964 from Patent WO0138577.
ACCESSION AX153049
VERSION AX153049.1 GI:14534700
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcripts
JOURNAL Patent: WO 0138577-A 964 31-MAY-2001;
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  Location/Qualifiers
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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
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  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 628 GTGCTGGA 635
  |||||
  1 GTGCTGGA 8

RESULT 130
LOCUS AX301528 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 242 from Patent WO0185941.
ACCESSION AX301528
VERSION AX301528.1 GI:17382611
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Versteeg R. and Caron, H.N.
TITLE MYC targets
JOURNAL Patent: WO 0185941-A 242 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             source
  Location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 40.0%; Score 8; DB 1; Length 10;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 AAAGAAAG 628
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  8 AAAGAAAG 1

RESULT 131
LOCUS BD065358 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065358
VERSION BD065358.1 GI:22610961
KEYWORDS JP 2001509017-A/294.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 10)
Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
Characterization of the yeast transcriptome
Patent: JP 2001509017-A 294 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT OS Saccharomyces cerevisiae (yeast)
FN JP 2001509017-A/294
PD 10-JUL-2001
PR 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU, BERT VOGELSTEIN, KENNETH W KINZLER PC
C12N15/10, C12N15/31, C07K14/395, C12Q1/68, C12Q1/02 CC
Characterization of the yeast transcriptome
FH 'Key' Location/Qualifiers
FT source 1..10

FEATURES             source
  The Johns Hopkins University (US)
  Location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 40.0%; Score 8; DB 1; Length 10;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
  |||||
  3 AAAAGAAA 10

RESULT 132
LOCUS CQ835815 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 873 from Patent WO2004059001.
ACCESSION CQ835815
VERSION CQ835815.1 GI:50835349
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn, D., Schlotmann, K., Gassenmeier, T., Holtkoetter, O.,
Conradt, M. and Hofmann, K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 873 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             source
  Location/Qualifiers
    1..11
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 26.0%; Score 5.2; DB 1; Length 11;
  Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 623 AGAAAGTGCT 632
  |||||
  11 AGAACTTTCT 2

Search completed: April 15, 2005, 12:52:20
Job time : 1 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 13:11:58 ; Search time 0.001 Seconds
(without alignments)
3.120 Million cell updates/sec

Title: US-10-619-220-65
Perfect score: 20
Sequence: 1 ccggaagaagaagtgtgga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched:

9 seqs, 78 residues
Total number of hits satisfying chosen parameters: 18

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 9 summaries

Database : us10619220-65.rst.subdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
C 1	9.4	47.0	11	CF543159
C 2	9.4	47.0	11	ACCESSION:CF543159
C 3	6.4	32.0	8	AL046337
C 4	6.4	32.0	8	AL046337
C 5	6.4	32.0	8	CF277997
C 6	6.4	32.0	8	CF301888
C 7	6.4	32.0	8	CF302851
C 8	6.4	32.0	8	CF312818
C 9	6.4	32.0	8	CF312818
				ACCESSION:CN763421
				ACCESSION:CL887698

ALIGNMENTS

RESULT 1
CF543159/c
LOCUS
DEFINITION
024-030-006 5-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 11)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wuck, W., Menze, A., O'Brien, J., Leirach, H. and Radelof, U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE
PUBMED
COMMENT

Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 30 row: 0 column: 06
Seq primer: SP6.

FEATURES

Location/Qualifiers
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/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:936619"
/db_xref="taxon:161934"
/clone="024-030-006"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 622 AAGAAAGTGTCT 632

Db 11 AAGAAAGTGT 1

RESULT 2

CL877169
LOCUS
DEFINITION
abf16b10.x1 Soybean random, unfiltered genomic library Glycine max genomic, genomic survey sequence.
CL877169 11 bp DNA linear GSS 30-AUG-2004
CL877169
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

1 (bases 1 to 11)
Nunberg, A., Bedell, J.A., Citek, R.W., Robbins, D., McMenamy, J., Peterson, S., Jones, J., Fries, J., Budiman, M.A., Nguyen, H. and Stacey, G.

Methylation filtered genomic sequences from Glycine max Unpublished (2004)
Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-1267
Fax: 573-882-0588
Email: stacey@missouri.edu
LIDID: 230
Class: shotgun.

TITLE

JOURNAL

COMMENT

FEATURES

Location/Qualifiers

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/organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="Young leaves"
/clone_lib="Soybean random, unfiltered genomic library"
/note="Vector: pOT2; Site 1: BstXI; Randomly sheared
genomic DNA ranging from 0.7-1.5 kb were end repaired and
ligated to BstXI linkers prior to cloning in BstXI-cut
pOT2. LibID: 230"

Query Match      47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 625 AAGTGCTGGA 635
Db 1 AATGTGCTGGA 11

RESULT 3
AL046337/c      8 bp mRNA linear EST 06-JUL-2004
LOCUS
DEFINITION DKF2p434J217.s1.434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION AL046337
VERSION AL046337.1 GI:49682663
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 8)
Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1. .8
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2p434J217"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

Query Match      32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 8 AAAAAAAA 1

RESULT 4
CF277997/c      8 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL-03-L19,
mRNA sequence.
ACCESSION CF277997
VERSION CF277997.1 GI:33655383
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

source
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/organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="Young leaves"
/clone_lib="Soybean random, unfiltered genomic library"
/note="Vector: pOT2; Site 1: BstXI; Randomly sheared
genomic DNA ranging from 0.7-1.5 kb were end repaired and
ligated to BstXI linkers prior to cloning in BstXI-cut
pOT2. LibID: 230"

Query Match      47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 625 AAGTGCTGGA 635
Db 1 AATGTGCTGGA 11

RESULT 3
AL046337/c      8 bp mRNA linear EST 06-JUL-2004
LOCUS
DEFINITION DKF2p434J217.s1.434 (synonym: htes3) Homo sapiens cDNA clone
ACCESSION AL046337
VERSION AL046337.1 GI:49682663
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 8)
Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

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/mol_type="mRNA"
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/clone="DKF2p434J217"
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/dev_stage="adult"
/lab_host="DH10B"
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Query Match      32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 8 AAAAAAAA 1

RESULT 4
CF277997/c      8 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL-03-L19,
mRNA sequence.
ACCESSION CF277997
VERSION CF277997.1 GI:33655383
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14ETL-03-L19"
/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 8 AAAAAAAA 1

RESULT 5
CF301888
LOCUS
DEFINITION 7LEAF--06-017.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-017, mRNA
sequence.
ACCESSION CF301888
VERSION CF301888.1 GI:33673649
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--06-017"
/tissue_type="leaf"

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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
|||||
1 AAAAAAA 8

RESULT 6
CF302851
LOCUS
DEFINITION
7LEAF--08-M07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--08-M07, mRNA
sequence.
ACCESSION
CF302851
VERSION
CF302851.1 GI:33674612
KEYWORDS
EST.
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--08-L15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--08-L15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

FEATURES
source
QY 620 AAAAGAAA 627
|||||
1 AAAAAAA 8
Db

RESULT 8
CN763421/c
LOCUS
DEFINITION
ID0AAA7AA11RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA7AA11 5',
mRNA sequence.
ACCESSION
CN763421
VERSION
CN763421.1 GI:47537344
KEYWORDS
EST.
SOURCE
Acyrthosiphon pisum (pea aphid)
ORGANISM
Acyrthosiphon pisum
Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 8)
Hunter,W., Martinez-Torres,D., Rabhe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.
An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum
Unpublished (2004)
Contact: D. Tagu
INRA Rennes
UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid

```

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CF312818.1 GI:33684579
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..8
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--08-L15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
|||||
1 AAAAAAA 8
Db

RESULT 8
CN763421/c
LOCUS
DEFINITION
ID0AAA7AA11RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA7AA11 5',
mRNA sequence.
ACCESSION
CN763421
VERSION
CN763421.1 GI:47537344
KEYWORDS
EST.
SOURCE
Acyrthosiphon pisum (pea aphid)
ORGANISM
Acyrthosiphon pisum
Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 8)
Hunter,W., Martinez-Torres,D., Rabhe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.
An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum
Unpublished (2004)
Contact: D. Tagu
INRA Rennes
UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid

```

Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAAACAGCTATGACC

Plate: 7 Row: A Column: 11.

Location/Qualifiers

FEATURES

source

1. .8
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
/clone="ID0AAVAA11"
/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="Xil-Blue"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0AAA ; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University ;
Soil conditions: Soil ; Sowing date: 01/06/1999 ;
Harvesting date: 01/06/1999 ; Stress date: no stress ;
Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction. ; experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 32.0%; Score 6.4; DB 1; Length 8;

Best Local Similarity 87.5%; Pred. No. 0;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGRAA 627

Db 8 AAAAAAA 1

RESULT 9

CL887698

LOCUS

DEFINITION CL887698 8 bp DNA linear GSS 30-AUG-2004
abf8ec02.x1 Soybean random, unfiltered genomic library Glycine max
genomic, genomic survey sequence.

ACCESSION CL887698

VERSION CL887698.1 GI:51629775

KEYWORDS GSS.

SOURCE Glycine max (soybean)

ORGANISM

Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

1 (bases 1 to 8)

REFERENCE Nunberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J.,

Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and

Stacey,G.

Methylation filtered genomic sequences from Glycine max

Unpublished (2004)

CONTACT: Gary Stacey

University of Missouri

108 Waters Hall, Columbia, MO 65211, USA

Tel: 573-884-1267

Fax: 573-882-0588

Email: stacey@missouri.edu

LidID: 230

Class: shotgun.

Location/Qualifiers

FEATURES

source

1. .8
/organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="young leaves"
/clone_lib="Soybean random, unfiltered genomic library"
/note="Vector: pOT2; Site 1: BstXI; Randomly sheared
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ligated to BstXI linkers prior to cloning in BstXI-cut
pOT2. LibID: 230"

Query Match 32.0%; Score 6.4; DB 1; Length 8;

Best Local Similarity 87.5%; Pred. No. 0;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 625 AAAGTGCT 632

Db 1 AATGTGCT 8

Search completed: April 15, 2005, 13:11:58

Job time : 0.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 13:07:49 ; Search time 0.001 Seconds
(without alignments)
33.080 Million cell updates/sec

Title: US-10-619-220-65

Perfect score: 20

Sequence: 1 ccggaagaagatgtgga 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 67 seqs, 827 residues

Total number of hits satisfying chosen parameters: 134

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 67 summaries

Database : us10619220-65.rnpb.subdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	20	100.0	20	1	US-09-799-848-25
C 2	20	100.0	20	1	US-09-802-669-73
C 3	20	100.0	20	1	US-10-445-996-3
C 4	20	100.0	20	1	US-10-619-220-73
C 5	20	100.0	20	1	US-10-664-639A-114
C 6	20	100.0	20	1	US-10-679-761-76
C 7	11.4	57.0	13	1	US-09-510-378-206
C 8	11.4	57.0	13	1	US-09-798-260-15
C 9	11	55.0	12	1	US-10-257-017B-378545
C 10	11	55.0	13	1	US-10-257-017B-125011
C 11	11	55.0	13	1	US-10-257-017B-125012
C 12	11	55.0	13	1	US-10-257-017B-216769
C 13	11	55.0	13	1	US-10-257-017B-216770
C 14	10.4	52.0	12	1	US-10-257-017B-311275
C 15	10.4	52.0	12	1	US-10-257-017B-340781
C 16	10.4	52.0	12	1	US-10-257-017B-363823
C 17	10.4	52.0	13	1	US-10-257-017B-34607
C 18	10.4	52.0	13	1	US-10-257-017B-34608
C 19	10.4	52.0	13	1	US-10-257-017B-111487
C 20	10.4	52.0	13	1	US-10-257-017B-111488
C 21	10.4	52.0	13	1	US-10-257-017B-132299
C 22	10.4	52.0	13	1	US-10-257-017B-132300
C 23	10.4	52.0	13	1	US-10-257-017B-191389
C 24	10.4	52.0	13	1	US-10-257-017B-191390
C 25	10.4	52.0	13	1	US-10-257-017B-203105
C 26	10.4	52.0	13	1	US-10-257-017B-203106
C 27	10.4	52.0	13	1	US-10-257-017B-223477
C 28	10.4	52.0	13	1	US-10-257-017B-223478
C 29	10.4	52.0	13	1	US-10-257-017B-260853
C 30	10.4	52.0	13	1	US-10-257-017B-260854
C 31	10.4	52.0	13	1	US-10-257-017B-262559
C 32	10.4	52.0	13	1	US-10-257-017B-262560
C 33	10	50.0	10	1	US-10-652-361-3

ALIGNMENTS

RESULT 1

US-09-799-848-25/c

Sequence 25, Application US/09799848

Patent No. US2001004145A1

GENERAL INFORMATION:

APPLICANT: Monia, Brett

APPLICANT: Cook, Phillip

APPLICANT: Crooke, Stanley

APPLICANT: Wu, Hongjiang

APPLICANT: Lima, Walter

TITLE OF INVENTION: METHODS OF USING MAMMALIAN RNASE H AND COMPOSITIONS THEREOF

FILE REFERENCE: ISPH-0521

CURRENT FILING DATE: 2001-03-05

PRIOR FILING DATE: 1999-06-30

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 1998-12-02

PRIOR FILING DATE: 1997-12-04

PRIOR FILING DATE: 1999-12-01

PRIOR FILING DATE: 1998-08-31

PRIOR FILING DATE: 1997-04-21

PRIOR FILING DATE: 1994-06-21

PRIOR FILING DATE: 1991-12-24

PRIOR FILING DATE: 2000-03-01

Sequence 4, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 170, App
Sequence 335477,
Sequence 336892,
Sequence 337350,
Sequence 338899,
Sequence 343815,
Sequence 349500,
Sequence 350690,
Sequence 353453,
Sequence 379095,
Sequence 547, App
Sequence 973, App
Sequence 9, Appli
Sequence 58, Appl
Sequence 268, App
Sequence 796, App
Sequence 29, Appl
Sequence 106, App
Sequence 647, App
Sequence 1092, Ap
Sequence 1408, Ap
Sequence 256, App
Sequence 17, Appl
Sequence 595, App
Sequence 596, App
Sequence 1108, Ap
Sequence 284, App
Sequence 17, Appl
Sequence 83, Appl
Sequence 33, Appl
Sequence 13, Appl

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; PRIOR APPLICATION NUMBER: PCT/US98/13966
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/889,296
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 08/411,734
; PRIOR FILING DATE: 1995-04-03
; PRIOR APPLICATION NUMBER: US 08/007,996
; PRIOR FILING DATE: 1993-10-21
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mus sp.
US-09-799-848-25

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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      616 CCGGAAAGAAAGTGTGGA 635
Db      20 CCGGAAAGAAAGTGTGGA 1

RESULT 2
US-09-802-669-73/c
; Sequence 73, Application US/09802669
; Patent No. US2002004490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-802-669-73

Query Match          100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      616 CCGGAAAGAAAGTGTGGA 635
Db      20 CCGGAAAGAAAGTGTGGA 1

RESULT 3
US-10-445-996-3/c
; Sequence 3, Application US/10445996
; Publication No. US20040005618A1
; GENERAL INFORMATION:
; APPLICANT: Zhengrong Yu
; APPLICANT: Brenda F. Baker
; APPLICANT: John Wu
; TITLE OF INVENTION: Nuclease-Based Method for Detecting and Quantitating
; FILE REFERENCE: ISPH-0500
; CURRENT APPLICATION NUMBER: US/10/445,996
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; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/705,587
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense oligonucleotide
US-10-445-996-3

Query Match          100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      20 CCGGAAAGAAAGTGTGGA 1

RESULT 4
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; Sequence 73, Application US/10619220
; Publication No. US20040033979A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/10/619,220
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 09/802,669
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-619-220-73

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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      20 CCGGAAAGAAAGTGTGGA 1

RESULT 5
US-10-664-639A-114/c
; Sequence 114, Application US/10664639A
; Publication No. US20040137471A1
; GENERAL INFORMATION:
; APPLICANT: Vickers, Timothy
; APPLICANT: Koo, Seongjoon
; APPLICANT: Bennett, C. Frank
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Baker, Brenda F.
; TITLE OF INVENTION: Efficient Reduction of Target RNA's by Single- and
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/10/445,996
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FILE REFERENCE: ISIS0001-100 (CORE00027US)
; CURRENT APPLICATION NUMBER: US/10/664,639A
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 60/411,780
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(5)
; OTHER INFORMATION: 2'-O-methoxyethyl substitutions
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(20)
; OTHER INFORMATION: 2'-O-methoxyethyl substitutions
US-10-664-639A-114

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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 CCGGAAAGAAAGTGTCTGGA 1

RESULT 6
US-10-679-761-76/c
; Sequence 76, Application US/10679761
; Publication No. US20040248145A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Lima, Walter
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Methods of Using Mammalian RNase H and Compositions Thereof
; FILE REFERENCE: ISPH-0790
; CURRENT APPLICATION NUMBER: US/10/679,761
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US 10/358,439
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US 09/992,738
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/781,712
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 09/861,205
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 09/684,254
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/343,809
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 09/203,716
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/067,458
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: US 60/248,950
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/497,412
; PRIOR FILING DATE: 2003-08-21
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound

US-10-679-761-76

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 616 CCGGAAAGAAAGTGTCTGGA 635
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Db 20 CCGGAAAGAAAGTGTCTGGA 1

RESULT 7
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; Sequence 206, Application US/09510378
; Publication No. US20030165823A1
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; Miyada, Charles Garrett
; Hubbell, Earl A.
; Chee, Mark
; Fodor, Stephen P.A.
; Huang, Xiaohua C.
; Lipshutz, Robert J.
; Lobban, Peter E.
; Morris, Macdonald S.
; Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
; Detecting Cystic Fibrosis
; NUMBER OF SEQUENCES: 250
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/510,378
; APPLICATION NUMBER: US/09/510,378
; FILING DATE: 22-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/544,381
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/510,521
; FILING DATE: 02-AUG-1995
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
; SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-510-378-206

Query Match 57.0%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGAAAGTGCT 632
13 AAAAGAAAGTACT 1

Db

RESULT 8
US-09-798-260-15/C
; Sequence 15, Application US/09798260
; Publication No. US20030165830A1
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles G.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Chee, Mark
; APPLICANT: Fodor, Stephen P. A.
; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, MacDonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: ARRAYS OF NUCLEIC ACID PROBES FOR ANALYZING
; FILE REFERENCE: 018547-015720US
; CURRENT APPLICATION NUMBER: US/09/798,260
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 08/778,794
; PRIOR FILING DATE: 1997-01-03
; PRIOR APPLICATION NUMBER: US 08/544,381
; PRIOR FILING DATE: 1995-10-10
; PRIOR APPLICATION NUMBER: US 08/510,521
; PRIOR FILING DATE: 1995-08-02
; PRIOR APPLICATION NUMBER: WO PCT/US94/12305
; PRIOR FILING DATE: 1994-10-26
; PRIOR APPLICATION NUMBER: US 08/284,064
; PRIOR FILING DATE: 1994-08-02
; PRIOR APPLICATION NUMBER: US 08/143,312
; PRIOR FILING DATE: 1993-10-26
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-798-260-15

Query Match 57.0%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGAAAGTGCT 632
13 AAAAGAAAGTACT 1

Db

RESULT 9
US-10-257-017B-378545
; Sequence 378545, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07

; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 378545
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0062833
US-10-257-017B-378545

Query Match 55.0%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAAGAAAGT 629
1 GAAAAGAAAGT 11

Db

RESULT 10
US-10-257-017B-125011
; Sequence 125011, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 125011
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0031240
US-10-257-017B-125011

Query Match 55.0%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAAGTG 630
2 AAAAGAAAGTG 12

Db

RESULT 11
US-10-257-017B-125012/C
; Sequence 125012, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 125012
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence

```
;
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0031240
US-10-257-017B-125012

Query Match      55.0%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      620 AAAAGAAAGTG 630
Db      12 AAAAGAAAGTG 2

RESULT 12
US-10-257-017B-216769
; Sequence 216769, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 216769
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052691
US-10-257-017B-216769

Query Match      55.0%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      618 GGAAGAAAG 628
Db      2 GGAAGAAAG 12

RESULT 13
US-10-257-017B-216770/c
; Sequence 216770, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 216770
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0052691
US-10-257-017B-216770

Query Match      55.0%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      618 GGAAGAAAG 628
Db      12 GGAAGAAAG 2

RESULT 14
US-10-257-017B-311275/c
; Sequence 311275, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 311275
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0024387
US-10-257-017B-311275

Query Match      52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 20;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      619 GAAAGAAAGTG 630
Db      12 GTRAGAAAGTG 1

RESULT 15
US-10-257-017B-340781/c
; Sequence 340781, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 340781
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0041677
US-10-257-017B-340781

Query Match      52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 20;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      618 GGAAGAAAGTG 629
Db      12 GGAAGAAAGTG 1

RESULT 16
```

```

US-10-257-017B-363823/c
; Sequence 363823, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 363823
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0054076
US-10-257-017B-363823

Query Match 52.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 20;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAAAGAAAGTC 631
Db 12 AAAAAAGAAATGC 1

RESULT 17
US-10-257-017B-34607
; Sequence 34607, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 34607
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011028
US-10-257-017B-34607

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAAAGAAAGT 629
Db 2 GGAAGAAAGAAAGT 13

RESULT 18
US-10-257-017B-34608/c
; Sequence 34608, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 34608
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011028
US-10-257-017B-34608

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAAAGAAAGT 629
Db 1 GGAAGAAAGAAAT 12

RESULT 20
US-10-257-017B-111488/c
; Sequence 111488, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111488
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027841
US-10-257-017B-111487

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAAAGAAAGT 629
Db 1 GGAAGAAAGAAAT 12

RESULT 19
US-10-257-017B-111487
; Sequence 111487, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111487
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027841
US-10-257-017B-111487

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAAAGAAAGT 629
Db 12 GGAAGAAAGAACT 1

```

; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111488
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027841
US-10-257-017B-111488

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAGAAAGT 629
| | | | | | | | | | | | |
Db 13 GGAAGAGAAAGT 2

RESULT 21

US-10-257-017B-132299
; Sequence 132299, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 132299
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033007
US-10-257-017B-132299

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAGAAAGT 629
| | | | | | | | | | | | |
Db 1 GGAAGAGAAAGT 12

RESULT 22

US-10-257-017B-132300/c
; Sequence 132300, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 132300
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033007
US-10-257-017B-132300

US-10-257-017B-132300

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAGAAAGT 629
| | | | | | | | | | | | |
Db 13 GGAAGAGAAAGT 2

RESULT 23

US-10-257-017B-191389
; Sequence 191389, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 191389
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047093
US-10-257-017B-191389

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 622 AAGAAAGTGCTG 633
| | | | | | | | | | | | |
Db 1 AAGAAAGTGCTG 12

RESULT 24

US-10-257-017B-191390/c
; Sequence 191390, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 191390
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047093
US-10-257-017B-191390

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 622 AAGAAAGTGCTG 633

```
Db      13 AAGAAAGTGTG 2
|||||
RESULT 25
US-10-257-017B-203105
; Sequence 203105, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 203105
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0049883
US-10-257-017B-203105
Query Match      52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      619 GAAAGAAAGTGTG 630
|||||
Db      2 GAATGAAGTGTG 13
|||||

RESULT 26
US-10-257-017B-203106/c
; Sequence 203106, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 203106
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0049883
US-10-257-017B-203106
Query Match      52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      619 GAAAGAAAGTGTG 630
|||||
Db      12 GAATGAAGTGTG 1
|||||

RESULT 27
US-10-257-017B-223477
; Sequence 223477, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 223477
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054405
US-10-257-017B-223477
Query Match      52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      618 GGAAGAAAGTGTG 629
|||||
Db      13 GGAAGAAAGTGTG 2
|||||

RESULT 28
US-10-257-017B-223478/c
; Sequence 223478, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 223478
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054405
US-10-257-017B-223478
Query Match      52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      618 GGAAGAAAGTGTG 629
|||||
Db      13 GGAAGAAAGTGTG 2
|||||

RESULT 29
US-10-257-017B-260853
; Sequence 260853, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 260853
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054405
US-10-257-017B-260853
Query Match      52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      618 GGAAGAAAGTGTG 629
|||||
Db      13 GGAAGAAAGTGTG 2
|||||
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 260853
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0063330
US-10-257-017B-260853

Query Match      52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAAGAAAGTGTG 630
Db 1 GAAAGAGATAGTG 12

RESULT 30
US-10-257-017B-260854/c
; Sequence 260854, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 260854
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0063330
US-10-257-017B-260854

Query Match      52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAAGAAAGTGTG 630
Db 13 GAAAGAGATAGTG 2

RESULT 31
US-10-257-017B-262559
; Sequence 262559, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 262559
```

```
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0063693
US-10-257-017B-262559

Query Match      52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAAAGTGTG 629
Db 2 GGAAGAAAGTGTG 13

RESULT 32
US-10-257-017B-262560/c
; Sequence 262560, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 262560
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0063693
US-10-257-017B-262560

Query Match      52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAAAGTGTG 629
Db 12 GGAAGAAAGTGTG 1

RESULT 33
US-10-652-361-3
; Sequence 3, Application US/10652361
; Publication No. US20050048498A1
; GENERAL INFORMATION:
; APPLICANT: WOUDEBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES
; FILE REFERENCE: 5049 US
; CURRENT APPLICATION NUMBER: US/10/652,361
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
```

us10619220-65.rnpb.sl

Fri Apr 15 13:23:04 2005

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-361-3

Query Match 50.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
|||||
DB 1 GAAAGAAAG 10

RESULT 34

US-10-652-361-4/c
; Sequence 4, Application US/10652361
; Publication No. US20050048498A1
; GENERAL INFORMATION:
; APPLICANT: WOUDEBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES
; FILE REFERENCE: 5049 US
; CURRENT APPLICATION NUMBER: US/10/652,361
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-361-4

Query Match 50.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
|||||
DB 10 GAAAGAAAG 1

RESULT 35

US-10-651-561-3
; Sequence 3, Application US/10651561
; Publication No. US20050069895A1
; GENERAL INFORMATION:
; APPLICANT: WOUDEBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; APPLICANT: HYLDIG-NIELSEN, JENS J.
; APPLICANT: SCHROEDER, BENJAMIN
; APPLICANT: VATTA, PAOLO
; APPLICANT: BLOCH, WILLIAM
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR DETECTING CODED
; TITLE OF INVENTION: MOLECULAR TAGS
; FILE REFERENCE: 5040 US
; CURRENT APPLICATION NUMBER: US/10/651,561
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-651-561-3

Query Match 50.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
|||||
DB 1 GAAAGAAAG 10

RESULT 36

US-10-651-561-4/c
; Sequence 4, Application US/10651561
; Publication No. US20050069895A1
; GENERAL INFORMATION:
; APPLICANT: WOUDEBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; APPLICANT: HYLDIG-NIELSEN, JENS J.
; APPLICANT: SCHROEDER, BENJAMIN
; APPLICANT: VATTA, PAOLO
; APPLICANT: BLOCH, WILLIAM
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR DETECTING CODED
; TITLE OF INVENTION: MOLECULAR TAGS
; FILE REFERENCE: 5040 US
; CURRENT APPLICATION NUMBER: US/10/651,561
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-651-561-4

Query Match 50.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
|||||
DB 10 GAAAGAAAG 1

RESULT 37

US-10-450-797-170
; Sequence 170, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conrad, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170
; LENGTH: 11

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-170

Query Match      50.0%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 AAAGAAAGTG 630
Db 1 AAAGAAAGTG 10

RESULT 38
US-10-257-017B-335477
; Sequence 335477, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 335477
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0038849
US-10-257-017B-335477

Query Match      50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAGAAAGT 629
Db 1 AAAGAAAGT 10

RESULT 39
US-10-257-017B-336892/c
; Sequence 336892, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 336892
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039574
US-10-257-017B-336892

Query Match      50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 619 GAAAGAAAG 628
Db 11 GAAAGAAAG 2

RESULT 40
US-10-257-017B-337350
; Sequence 337350, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 337350
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039831
US-10-257-017B-337350

Query Match      50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 GGAAGAAAG 627
Db 3 GGAAGAAAG 12

RESULT 41
US-10-257-017B-338899
; Sequence 338899, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 338899
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005508
US-10-257-017B-338899

Query Match      50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
Db 2 GAAAGAAAG 11

RESULT 42
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Fri Apr 15 13:23:04 2005

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US-10-257-017B-343815
; Sequence 343815, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 343815
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0006945
US-10-257-017B-343815

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAAGT 629
DB 3 AAAAGAAAGT 12

RESULT 43
US-10-257-017B-349500/c
; Sequence 349500, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 349500
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046174
US-10-257-017B-349500

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAAGT 629
DB 12 AAAAGAAAGT 3

RESULT 44
US-10-257-017B-350690
; Sequence 350690, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 350690
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048525
US-10-257-017B-350690

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 GGAAGAGAAA 627
DB 1 GGAAGAGAAA 10

RESULT 45
US-10-257-017B-353453
; Sequence 353453, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 353453
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048525
US-10-257-017B-353453

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 GGAAGAGAAA 627
DB 1 GGAAGAGAAA 10

RESULT 46
US-10-257-017B-379095/c
; Sequence 379095, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 379095
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048525
US-10-257-017B-379095/c

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```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 379095
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004612
US-10-257-017B-379095

Query Match          50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAAGT 629
Db 12 AAAAGAAAGT 3

RESULT 47
US-10-450-797-547
; Sequence 547, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 547
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-547

Query Match          47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAAGAAAGT 629
Db 1 GAAAGTAAAGT 11

RESULT 48
US-10-450-797-973
; Sequence 973, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 973
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-10-450-797-973

Query Match          47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAAGAAAGT 629
Db 1 GAAACAAAGT 11

RESULT 49
US-10-645-187-9/C
; Sequence 9, Application US/10645187
; Publication No. US20040191222A1
; GENERAL INFORMATION:
; APPLICANT: Emini, Emilio A.
; APPLICANT: Shiver, John W.
; APPLICANT: Bett, Andrew J.
; APPLICANT: Casimiro, Danilo R.
; APPLICANT: Kaslow, David C.
; APPLICANT: Chastain, Michael
; TITLE OF INVENTION: ADENOVIRUS SEROTYPE 34 VECTORS, NUCLEIC
; FILE REFERENCE: 21390
; CURRENT APPLICATION NUMBER: US/10/645,187
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/458,825
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: adenovirus serotype 34
US-10-645-187-9

Query Match          47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 623 AGAAAGTGTG 633
Db 11 AGAAAGTGCGG 1

RESULT 50
US-09-979-593-58
; Sequence 58, Application US/09979593
; Publication No. US20030082555A1
; GENERAL INFORMATION:
; APPLICANT: Genessee Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y
; APPLICANT: Denton, R. Rex
; APPLICANT: Kliem, Stefanie E
; APPLICANT: Lee, Helen H
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
; FILE REFERENCE: MWH-0425 PCT ICAM2
; CURRENT APPLICATION NUMBER: US/09/979,593
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/14714
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: 60/201,946
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 10
; TYPE: DNA
```

```
; ORGANISM: Homo sapien
US-09-979-593-58

Query Match      45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      626 AAGTGCTGG 634
Db      2 AAGTGCTGG 10

RESULT 51
US-10-223-765-268
; Sequence 268, Application US/10223765
; Publication No. US20030165997A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-223-765-268

Query Match      45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      619 GAAAGAGAAA 627
Db      2 GAAAGAGAAA 10

RESULT 52
US-10-450-797-796
; Sequence 796, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 796
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-796

; ORGANISM: Homo sapien
US-09-945-505-29

Query Match      45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      619 GAAAGAGAAA 627
Db      3 GAAAGAGAAA 11

RESULT 53
US-09-945-505-29
; Sequence 29, Application US/09945505
; Publication No. US20030165844A1
; GENERAL INFORMATION:
; APPLICANT: Anastasio, Alison E.
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: Haplotypes of the TNFRSF1A Gene
; FILE REFERENCE: MMH-00300S
; CURRENT APPLICATION NUMBER: US/09/945,505
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-945-505-29

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      619 GAAAGAGAAA 628
Db      1 GTAAAGAGAA 10

RESULT 54
US-10-033-145-106/c
; Sequence 106, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 106
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-106

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      620 AAAAGAGAAAGT 629
Db      10 AAAAGAGATGT 1

RESULT 55
US-10-033-145-106/c
; Sequence 106, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 106
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-106

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      620 AAAAGAGAAAGT 629
Db      10 AAAAGAGATGT 1
```

```
RESULT 55
US-10-033-145-647
; Sequence 647, Application US/10033145
; Publication No. US200201515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; SOFTWARE: PatentIn version 3.0
; NUMBER OF SEQ ID NOS: 2137
; SEQ ID NO 647
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-647

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      617 CGGAAAAGAA 626
Db      1 CGGAAAAGGA 10
|||||

RESULT 56
US-10-033-145-1092/c
; Sequence 1092, Application US/10033145
; Publication No. US200201515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; SOFTWARE: PatentIn version 3.0
; NUMBER OF SEQ ID NOS: 2137
; SEQ ID NO 1092
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1092

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      617 CGGAAAAGAA 626
Db      1 CGGAAAAGGA 10
|||||

RESULT 57
US-10-033-145-1408
; Sequence 1408, Application US/10033145
; Publication No. US200201515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; SOFTWARE: PatentIn version 3.0
; NUMBER OF SEQ ID NOS: 2137
; SEQ ID NO 1408
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1408

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      617 CGGAAAAGAA 626
Db      1 CGGAAAAGGA 10
|||||

RESULT 58
US-10-223-765-256
; Sequence 256, Application US/10223765
; Publication No. US20030165997A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-223-765-256

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      617 CGGAAAAGAA 626
Db      1 CGGAAAAGAA 10
|||||

RESULT 59
US-10-390-045-17
; Sequence 17, Application US/10390045
; Publication No. US20030170713A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US/09/769,482
US-10-390-045-17

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      617 CGGAAAAGAA 626
Db      1 CGGAAAAGAA 10
|||||
```

```
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-390-045-17

Query Match          42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      619 GAAAGAGAGG 628
Db      1 GAAAGAGAGG 10
|||||

RESULT 60
US-10-330-627-595
; Sequence 595, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; CURRENT APPLICATION NUMBER: US/10/330,627
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 595
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-595

Query Match          42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      618 GGAAGAGAAA 627
Db      1 GGAAGAGAAA 10
|||||

RESULT 61
US-10-330-627-596
; Sequence 596, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 596
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-596

Query Match          42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      618 GGAAGAGAAA 627
Db      1 GGAAGAGAAA 10
|||||

RESULT 62
US-10-330-627-1108
; Sequence 1108, Application US/10330627
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1108
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1108

Query Match          42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      620 AAAAGAGAGT 629
Db      1 AAAAGAGAGT 10
|||||

RESULT 63
US-10-091-281-284
; Sequence 284, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 284
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative HEAT/HSF1.01 motif
US-10-091-281-284

Query Match          42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      623 AGAAGAGTGT 632
Db      1 AGAAGAGTGT 632
|||||
```

Db 1 AGAAGTTCT 10

RESULT 64

US-10-434-479-17

Sequence 17, Application US/10434479

Publication No. US20040092469A1

GENERAL INFORMATION:

APPLICANT: SRIVASTAVA, SHIV

APPLICANT: MOUL, JUDD W.

APPLICANT: XU, LINDA L.

TITLE OF INVENTION: ANDROGEN-REGULATED PMP21 GENE AND POLYPEPTIDES

FILE REFERENCE: 04995, 0057-02000

CURRENT APPLICATION NUMBER: US/10/434,479

CURRENT FILING DATE: 2003-05-09

PRIOR APPLICATION NUMBER: 10/390,045

PRIOR FILING DATE: 2003-03-18

PRIOR APPLICATION NUMBER: 09/769,482

PRIOR FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/178,772

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/179,045

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 81

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 17

LENGTH: 10

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: oligonucleotide

US-10-434-479-17

Query Match 42.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 33;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAAGGAAG 628

Db 1 GAAAGGAAG 10

RESULT 65

US-10-660-253-83

Sequence 83, Application US/10660253

Publication No. US20040115705A1

GENERAL INFORMATION:

APPLICANT: Behlke, Mark A.

APPLICANT: Lingyan, Huang

APPLICANT: Owczarzy, Richard

APPLICANT: Walder, Joseph A.

TITLE OF INVENTION: METHODS AND SYSTEMS FOR ESTIMATING THE MELTING TEMPERATURE (Tm) OF POLYNUCLEOTIDE MOLECULES

FILE REFERENCE: 03988/100K297-US1

CURRENT APPLICATION NUMBER: US/10/660,253

CURRENT FILING DATE: 2003-09-11

PRIOR APPLICATION NUMBER: US 60/410,663

PRIOR FILING DATE: 2002-09-12

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 83

LENGTH: 10

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: oligonucleotide

US-10-660-253-83

Query Match 42.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 33;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAAGGAAG 628

Db 1 GAAAGGAAG 10

RESULT 66

US-10-487-934-33

Sequence 33, Application US/10487934

Publication No. US20040265824A1

GENERAL INFORMATION:

APPLICANT: Buckhaults, Phillip

APPLICANT: Kinzler, Kenneth

APPLICANT: Vogelstein, Bert

TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS

FILE REFERENCE: 001107.00429

CURRENT APPLICATION NUMBER: US/10/487,934

CURRENT FILING DATE: 2004-03-03

PRIOR APPLICATION NUMBER: 60/317,494

PRIOR FILING DATE: 2001-09-07

PRIOR APPLICATION NUMBER: 60/383,805

PRIOR FILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 334

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 33

LENGTH: 10

TYPE: DNA

ORGANISM: Homo sapiens

US-10-487-934-33

Query Match 42.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 33;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGAAAGT 629

Db 1 AAAAGAAAGT 10

RESULT 67

US-10-755-118-13/c

Sequence 13, Application US/10755118

Publication No. US2005009041A1

GENERAL INFORMATION:

APPLICANT: Buchardt, Ole

APPLICANT: Egholm, Michael

APPLICANT: Nielsen, Peter Eigil

APPLICANT: Berg, Rolf Henrik

TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS AND SYNTHETIC PROCEDURES THEREFOR

FILE REFERENCE: ISIS-5427

CURRENT APPLICATION NUMBER: US/10/755,118

CURRENT FILING DATE: 2004-01-09

PRIOR APPLICATION NUMBER: US 08/462,977

PRIOR FILING DATE: 1995-06-05

PRIOR APPLICATION NUMBER: US 08/108,591

PRIOR FILING DATE: 1993-11-22

PRIOR APPLICATION NUMBER: PCT/EP92/01219

PRIOR FILING DATE: 1992-05-22

PRIOR APPLICATION NUMBER: DN 510/92

PRIOR FILING DATE: 1992-04-15

PRIOR APPLICATION NUMBER: DN 987/91

PRIOR FILING DATE: 1991-05-24

PRIOR APPLICATION NUMBER: DN 986/91

PRIOR FILING DATE: 1991-05-24

NUMBER OF SEQ ID NOS: 157

SOFTWARE: PatentIn version 3.2

SEQ ID NO 13

LENGTH: 10

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Construct

US-10-755-118-13

Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 33;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 618 GGAAAGAAA 627
 |||||
 Db 10 GGAAAAAAAA 1

Search completed: April 15, 2005, 13:07:49
 Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 13:04:09 ; Search time 0.001 Seconds
(without alignments)
42.160 Million cell updates/sec

Title: US-10-619-220-65

Perfect score: 20
Sequence: 1 cgggaaagaaagtgtgga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 99 seqs, 1054 residues

Total number of hits satisfying chosen parameters: 198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 99 summaries

Database : us10619220-65.rni.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	20	1	US-09-290-640-73
C 2	20	100.0	20	1	US-09-665-615B-73
C 3	12.4	62.0	15	1	US-08-319-492B-8
C 4	12.4	62.0	15	1	US-08-319-492B-9
C 5	11.4	57.0	13	1	US-08-544-381B-206
C 6	11.4	57.0	13	1	US-08-778-794A-15
C 7	11.4	57.0	13	1	US-09-341-399-15
C 8	10	50.0	12	1	US-08-004-800-9
C 9	10	50.0	12	1	US-08-004-800-10
C 10	10	50.0	12	1	US-08-413-813-9
C 11	10	50.0	12	1	US-08-413-813-10
C 12	10	50.0	12	1	US-08-413-813-28
C 13	10	50.0	12	1	US-08-413-813-29
C 14	10	50.0	12	1	US-08-413-813-31
C 15	10	50.0	12	1	US-08-173-489C-215
C 16	10	50.0	12	1	US-08-467-346-9
C 17	10	50.0	12	1	US-08-467-346-10
C 18	10	50.0	12	1	US-08-467-346-28
C 19	10	50.0	12	1	US-08-467-346-29
C 20	10	50.0	12	1	US-08-467-346-31
C 21	10	50.0	12	1	PCT-US92-02480A-9
C 22	10	50.0	12	1	PCT-US92-02480A-10
C 23	9.4	47.0	11	1	US-08-173-489C-239
C 24	9.4	47.0	11	1	US-09-475-947A-96
C 25	9	45.0	10	1	US-08-173-489C-67
C 26	9	45.0	10	1	US-09-475-947A-120
C 27	9	45.0	10	1	US-09-534-366A-13
C 28	9	45.0	11	1	US-08-173-489C-73
C 29	8.4	42.0	10	1	US-08-173-489C-153
C 30	8.4	42.0	10	1	US-08-173-489C-203
C 31	8.4	42.0	10	1	US-09-508-753B-48
C 32	8.4	42.0	10	1	US-09-508-753B-71
C 33	8.4	42.0	10	1	US-09-769-482-17

34	8.4	42.0	10	1	5422251-4	Patent No. 5422251
35	8.4	42.0	10	1	5422251-4	Sequence 16, Appl
c 36	8.2	41.0	10	1	US-08-737-371A-16	Sequence 17, Appl
c 37	8.2	41.0	10	1	US-08-737-371A-17	Sequence 16, Appl
c 38	8.2	41.0	10	1	PCT-US95-05853-16	Sequence 17, Appl
c 39	8.2	41.0	10	1	PCT-US95-05853-17	Sequence 17, Appl
c 40	8	40.0	8	1	US-08-662-963-17	Sequence 17, Appl
c 41	8	40.0	9	1	US-09-442-054A-67	Sequence 78, Appl
c 42	8	40.0	9	1	US-09-442-054A-78	Sequence 86, Appl
c 43	8	40.0	9	1	US-09-442-054A-86	Sequence 4, Appl
c 44	8	40.0	10	1	US-08-088-658-4	Sequence 43, Appl
c 45	8	40.0	10	1	US-08-088-658-43	Sequence 49, Appl
c 46	8	40.0	10	1	US-08-686-116A-49	Sequence 51, Appl
c 47	8	40.0	10	1	US-08-686-116A-51	Sequence 49, Appl
c 48	8	40.0	10	1	US-08-685-484-49	Sequence 51, Appl
c 49	8	40.0	10	1	US-08-685-484-51	Sequence 49, Appl
c 50	8	40.0	10	1	US-08-847-108-49	Sequence 51, Appl
c 51	8	40.0	10	1	US-08-847-108-51	Sequence 56, Appl
c 52	8	40.0	10	1	US-08-686-113A-56	Sequence 58, Appl
c 53	8	40.0	10	1	US-08-686-113A-58	Sequence 49, Appl
c 54	8	40.0	10	1	US-08-847-095A-49	Sequence 51, Appl
c 55	8	40.0	10	1	US-08-847-095A-51	Sequence 4, Appl
c 56	8	40.0	10	1	US-08-471-907A-4	Sequence 43, Appl
c 57	8	40.0	10	1	US-08-471-907A-43	Sequence 272, App
c 58	8	40.0	10	1	US-08-388-353-272	Sequence 273, App
c 59	8	40.0	10	1	US-08-388-353-273	Sequence 274, App
c 60	8	40.0	10	1	US-08-388-353-274	Sequence 272, App
c 61	8	40.0	10	1	US-08-488-551B-272	Sequence 273, App
c 62	8	40.0	10	1	US-08-488-551B-273	Sequence 274, App
c 63	8	40.0	10	1	US-08-488-551B-274	Sequence 1, Appl
c 64	8	40.0	10	1	US-08-857-721-1	Sequence 20, Appl
c 65	8	40.0	10	1	US-08-088-661F-20	Sequence 22, Appl
c 66	8	40.0	10	1	US-08-088-661F-22	Sequence 241, App
c 67	8	40.0	10	1	US-08-899-241-241	Sequence 2, Appl
c 68	8	40.0	10	1	US-08-150-156A-2	Sequence 5, Appl
c 69	8	40.0	10	1	US-08-150-156A-5	Sequence 14, Appl
c 70	8	40.0	10	1	US-08-150-156A-14	Sequence 16, Appl
c 71	8	40.0	10	1	US-08-150-156A-16	Sequence 8, Appl
c 72	8	40.0	10	1	US-08-108-591B-8	Sequence 9, Appl
c 73	8	40.0	10	1	US-08-108-591B-9	Sequence 10, Appl
c 74	8	40.0	10	1	US-08-108-591B-10	Sequence 12, Appl
c 75	8	40.0	10	1	US-08-108-591B-12	Sequence 14, Appl
c 76	8	40.0	10	1	US-08-108-591B-14	Sequence 56, Appl
c 77	8	40.0	10	1	US-08-686-114B-56	Sequence 58, Appl
c 78	8	40.0	10	1	US-08-686-114B-58	Sequence 80, Appl
c 79	8	40.0	10	1	US-09-475-947A-80	Sequence 142, App
c 80	8	40.0	10	1	US-09-475-947A-142	Sequence 140, App
c 81	8	40.0	10	1	US-09-508-753B-140	Sequence 208, App
c 82	8	40.0	10	1	US-09-508-753B-208	Sequence 56, Appl
c 83	8	40.0	10	1	US-09-337-304-56	Sequence 58, Appl
c 84	8	40.0	10	1	US-09-337-304-58	Sequence 8, Appl
c 85	8	40.0	10	1	US-08-468-719A-8	Sequence 10, Appl
c 86	8	40.0	10	1	US-08-468-719A-10	Sequence 12, Appl
c 87	8	40.0	10	1	US-08-468-719A-12	Sequence 46, Appl
c 88	8	40.0	10	1	US-08-468-719A-14	Sequence 46, Appl
c 89	8	40.0	10	1	US-08-468-719A-46	Sequence 51, Appl
c 90	8	40.0	10	1	US-09-230-088-49	Sequence 8, Appl
c 91	8	40.0	10	1	US-09-230-088-51	Sequence 10, Appl
c 92	8	40.0	10	1	US-08-462-977B-8	Sequence 10, Appl
c 93	8	40.0	10	1	US-08-462-977B-10	Sequence 12, Appl
c 94	8	40.0	10	1	US-08-462-977B-12	Sequence 14, Appl
c 95	8	40.0	10	1	US-08-462-977B-14	Sequence 43, Appl
c 96	8	40.0	10	1	US-09-442-054A-43	Sequence 58, Appl
c 97	8	40.0	10	1	US-09-442-054A-58	Sequence 1, Appl
c 98	7.6	38.0	8	1	US-08-853-980-1	Sequence 33, Appl
c 99	7.4	37.0	9	1	US-09-375-673B-33	

ALIGNMENTS

RESULT 1
US-09-290-640-73/c

Sequence 73, Application US/09290640
Patent No. 6204055
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 73
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-290-640-73

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 616 CCGGAAAGAAAGTGTGGA 635
DB 20 CCGGAAAGAAAGTGTGGA 1

RESULT 2
US-09-665-615B-73/c
Sequence 73, Application US/09665615B
Patent No. 6653133
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
APPLICANT: Wyatt, Jacqueline
TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0502
CURRENT APPLICATION NUMBER: US/09/665,615B
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 179
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 73
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-665-615B-73

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 616 CCGGAAAGAAAGTGTGGA 635
DB 20 CCGGAAAGAAAGTGTGGA 1

RESULT 3
US-08-319-492B-8/c
Sequence 8, Application US/08319492B
Patent No. 5616488
GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,492B
FILING DATE: October 7, 1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application described below:
PRIOR APPLICATION DATA: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-319-492B-8

Query Match 62.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GCGAAAGAAAGTGC 631
DB 15 GCGAAAGAAAGTGC 2

RESULT 4
US-08-319-492B-9/c
Sequence 9, Application US/08319492B
Patent No. 5616488
GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

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; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-319-492B-9

Query Match 62.0%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAAGAAAGTGC 631
Db 14 GGCAAGAAAGTGC 1

RESULT 5
US-08-544-381B-206/c
; Sequence 206, Application US/08544381B
; Patent No. 6027880
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles Garrett
; APPLICANT: Miyada, Charles Garrett
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
; TITLE OF INVENTION: Detecting Cystic Fibrosis
; NUMBER OF SEQUENCES: 250
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/544,381B
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/510,521
; FILING DATE: 02-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-0041300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
;
US-08-544-381B-206

Query Match 57.0%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGAAAGTGC 632
Db 13 AAAAGAAAGTACT 1

RESULT 6
US-08-778-794A-15/c
; Sequence 15, Application US/08778794A
; Patent No. 6309823
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles Garrett
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Chee, Mark
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes
; TITLE OF INVENTION: for Analyzing Biotransformation Genes
; NUMBER OF SEQUENCES: 156
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,794A
; FILING DATE: 03-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312

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FILING DATE: 26-OCT-1993
APPLICATION NUMBER: US 08/284,064
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: WO PCT/US94/12305
FILING DATE: 26-OCT-1994
APPLICATION NUMBER: US 08/510,521
FILING DATE: 02-AUG-1995
APPLICATION NUMBER: US 08/544,381
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/778,794
FILING DATE: 03-JAN-1997
APPLICATION NUMBER: WO PCT/US98/06414
FILING DATE: 02-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-015700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-778-794A-15

Query Match 57.0%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGAAAGTGCT 632
Db 13 AAAAGAAAGTACT 1

RESULT 7
US-09-341-399-15/c
Sequence 15, Application US/09341399
Patent No. 6468744
GENERAL INFORMATION:
APPLICANT: Cronin, Maureen T.
Sheldon, Edward L.
Miyada, Charles G.
Hubbell, Earl A.
Chee, Mark
Fodor, Stephen P.A.
Huang, Xisohua C.
Lipshutz, Robert J.
Lobban, Peter E.
Morris, MacDonald S.
TITLE OF INVENTION: Analysis of Genetic Polymorphisms and Gene Copy Number
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/341.399
FILING DATE: 17-No. 6468744-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: US 08/284,064

FILING DATE: 02-AUG-1994
APPLICATION NUMBER: WO PCT/US94/12305
FILING DATE: 26-OCT-1994
APPLICATION NUMBER: US 08/510,521
FILING DATE: 02-AUG-1995
APPLICATION NUMBER: US 08/544,381
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/778,794
FILING DATE: 03-JAN-1997
APPLICATION NUMBER: WO PCT/US98/06414
FILING DATE: 02-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-015710US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-341-399-15

Query Match 57.0%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGAAAGTGCT 632
Db 13 AAAAGAAAGTACT 1

RESULT 8
US-08-004-800-9
Sequence 9, Application US/08004800
Patent No. 5426180
GENERAL INFORMATION:
APPLICANT: Kool, Eric T.
TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/004,800
FILING DATE: 19930111
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: McNulty, William E.
REGISTRATION NUMBER: 22,606
REFERENCE/DOCKET NUMBER: 80852Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs

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; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-004-800-9

Query Match          50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      619 GAAAGAAAG 628
Db      3 GAAAGAAAG 12

RESULT 9
US-08-004-800-10/c
; Sequence 10, Application US/08004800
; Patent No. 5426180
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/004,800
; FILING DATE: 19930111
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McNulty, William E.
; REGISTRATION NUMBER: 22,606
; REFERENCE/DOCKET NUMBER: 8085ZYX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-004-800-10

Query Match          50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      619 GAAAGAAAG 628
Db      10 GAAAGAAAG 1

RESULT 10
US-08-413-813-9
; Sequence 9, Application US/08413813
; Patent No. 5683874
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
```

```
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,813
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8085ZYX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-413-813-9

Query Match          50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      619 GAAAGAAAG 628
Db      3 GAAAGAAAG 12

RESULT 11
US-08-413-813-10/c
; Sequence 10, Application US/08413813
; Patent No. 5683874
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,813
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8085ZYX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
```

TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-413-813-10

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
|||||

Db 10 GAAAGAAAG 1

RESULT 12

US-08-413-813-28
; Sequence 28, Application US/08413813
; Patent No. 5683874
; GENERAL INFORMATION:

APPLICANT: KOOL, Eric T.
; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,813
FILING DATE:

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8085ZYX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-413-813-28

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
|||||

Db 1 GAAAGAAAG 10

RESULT 13

US-08-413-813-29
; Sequence 29, Application US/08413813
; Patent No. 5683874
; GENERAL INFORMATION:

APPLICANT: KOOL, Eric T.

; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,813
FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8085ZYX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-413-813-29

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
|||||

Db 1 GAAAGAAAG 10

RESULT 14

US-08-413-813-31/c
; Sequence 31, Application US/08413813
; Patent No. 5683874
; GENERAL INFORMATION:

APPLICANT: KOOL, Eric T.
; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,813
FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8085ZYX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343

```

; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; US-08-413-813-31

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
DB 12 GAAAGAAAG 3

RESULT 15
US-08-173-489C-215
; Sequence 215, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 238 rRNA gene from Escherichia coli
; DESCRIPTION: (Accession # M25458) nucleotides 212 to 223
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; STRAIN: MR6600
; PUBLICATION INFORMATION:
; AUTHORS: Branlant, C, Krol, A, Machatt, M, A,
; AUTHORS: Pouyet, J, Ebel, J P, Edwards, K, Koessel,
; AUTHORS: H.

; TITLE: Primary and secondary
; structures of Escherichia coli MRE 600 23S
; TITLE: ribosomal RNA Comparison with models of
; TITLE: secondary structure for maize chloroplast 23S
; TITLE: rRNA and for large portions of mouse and human
; TITLE: 16S mitochondrial rRNAs
; JOURNAL: Nucleic Acids Research
; VOLUME: 9
; PAGES: 4303-4324
; DATE: 1981
; RELEVANT RESIDUES IN SEQ ID NO: 215 :FROM 1 TO 12
; US-08-173-489C-215

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 GGAAAGAAAG 627
DB 3 GGAAAGAAAG 12

RESULT 16
US-08-467-346-9
; Sequence 9, Application US/08467346
; Patent No. 5872105
; GENERAL INFORMATION:
; APPLICANT: KOOL, Eric T.
; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,346
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/413,813
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 80852YX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-467-346-9

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
DB 3 GAAAGAAAG 12

```

```
RESULT 17
US-08-467-346-10/c
; Sequence 10, Application US/08467346
; Patent No. 5872105
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,346
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/413,813
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8085ZYX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4366
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-467-346-10

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
Db 10 GAAAGAAAG 1

RESULT 18
US-08-467-346-28
; Sequence 28, Application US/08467346
; Patent No. 5872105
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,346
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/413,813
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8085ZYX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4366
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-467-346-10

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
Db 10 GAAAGAAAG 1
```

```
RESULT 19
US-08-467-346-29
; Sequence 29, Application US/08467346
; Patent No. 5872105
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,346
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/413,813
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8085ZYX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4366
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-467-346-28

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
Db 1 GAAAGAAAG 10

RESULT 19
US-08-467-346-29
; Sequence 29, Application US/08467346
; Patent No. 5872105
; GENERAL INFORMATION:
; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,346
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/413,813
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8085ZYX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4366
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-467-346-28
```

US-08-467-346-29

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
|||||
Db 1 GAAAGAAAG 10

RESULT 20

US-08-467-346-31/c
; Sequence 31, Application US/08467346
; Patent No. 5872105
; GENERAL INFORMATION:

; APPLICANT: Kool, Eric T.
; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/467,346

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/413,813

; FILING DATE: 30-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Digiglio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 8085ZYX

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 742-4343

; TELEFAX: (516) 742-4366

; TELEX: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: circular

US-08-467-346-31

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
|||||
Db 12 GAAAGAAAG 3

RESULT 21

PCT-US92-02480A-9

; Sequence 9, Application PC/TUS9202480A

; GENERAL INFORMATION:

; APPLICANT: Kool, Eric T.

; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02480A
; FILING DATE: 19920326

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: McNulty, William E.

; REGISTRATION NUMBER: 22,606

; REFERENCE/DOCKET NUMBER: 8085Z

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 742-4343

; TELEFAX: (516) 742-4366

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

PCT-US92-02480A-9

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
|||||
Db 3 GAAAGAAAG 12

RESULT 22

PCT-US92-02480A-10/c

; Sequence 10, Application PC/TUS9202480A

; GENERAL INFORMATION:

; APPLICANT: Kool, Eric T.

; TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/02480A

; FILING DATE: 19920326

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: McNulty, William E.

; REGISTRATION NUMBER: 22,606

; REFERENCE/DOCKET NUMBER: 8085Z

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 742-4343

; TELEFAX: (516) 742-4366

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 base pairs

; TYPE: NUCLEIC ACID

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; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US92-02480A-10

Query Match      50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      619 GAAAGAAAG 628
Db      10 GAAAGAAAG 1

RESULT 23
US-08-173-489C-299
; Sequence 299, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELEPHONE: (attorney) (212) 246-8959
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 299:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 16s rRNA gene from Chlamydia psittaci
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Chlamydia psittaci
; PUBLICATION INFORMATION:
; AUTHORS: Weisburg, W G, Hatch, T P, Woese, C R.
; TITLE: Eubacterial Origin of
; TITLE: Chlamydiae
; JOURNAL: Journal of Bacteriology
; VOLUME: 167
; PAGES: 570-574
; DATE: 1986
; RELEVANT RESIDUES IN SEQ ID NO: 299 :FROM 1 TO 11
US-08-173-489C-299

Query Match      47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      618 GGAAAGAAAG 628
Db      1 GGAAAGAAAG 11

RESULT 24
US-09-475-947A-96
; Sequence 96, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 11
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-96

Query Match      47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      618 GGAAAGAAAG 628
Db      1 GGAAAGAAAG 11

RESULT 25
US-08-173-489C-67
; Sequence 67, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELEPHONE: (attorney) (212) 246-8959
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 299:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 16s rRNA gene from Chlamydia psittaci
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Chlamydia psittaci
; PUBLICATION INFORMATION:
; AUTHORS: Weisburg, W G, Hatch, T P, Woese, C R.
; TITLE: Eubacterial Origin of
; TITLE: Chlamydiae
; JOURNAL: Journal of Bacteriology
; VOLUME: 167
; PAGES: 570-574
; DATE: 1986
; RELEVANT RESIDUES IN SEQ ID NO: 299 :FROM 1 TO 11
US-08-173-489C-299

Query Match      47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      618 GGAAAGAAAG 628
Db      1 GGAAAGAAAG 11
```

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; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 base pairs
;   TYPE: Nucleic Acid
;   STRANDEDNESS: double stranded
;   TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; DESCRIPTION: esterase D gene (Accession # M13450)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: chromosome 13
; MAP POSITION: 13q14.1-q14.2
; PUBLICATION INFORMATION:
; AUTHORS: Lee, E Y H P, Lee, W H.
; TITLE: Molecular cloning of the
; TITLE: human esterase D gene, a genetic marker of
; JOURNAL: retinoblastoma
; JOURNAL: Proceedings of the National Academy of
; JOURNAL: Sciences, USA
; VOLUME: 83
; PAGES: 6337-6341
; DATE: 1986
; RELEVANT RESIDUES IN SEQ ID NO: 67 :FROM 1 TO 10
US-08-173-489C-67

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 GGAAGAAG 626
DB 2 GGAAGAAG 10

RESULT 26
US-09-475-947A-120
; Sequence 120, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-120

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAG 628
DB 2 AAAAGAAG 10

RESULT 27
US-09-534-366A-13
; Sequence 13, Application US/09534366A
; Patent No. 6759195
; GENERAL INFORMATION:
; APPLICANT: Bentley, William E.

; APPLICANT: Gill, Ryan T.
; TITLE OF INVENTION: Method of Differential Display of Prokaryotic Messenger
; FILE REFERENCE: RNA by RT-PCR
; CURRENT APPLICATION NUMBER: US/09/534,366A
; CURRENT FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PROV 60/126,038
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
US-09-534-366A-13

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 626 AAGTCTGG 634
DB 2 AAGTCTGG 10

RESULT 28
US-08-173-489C-73
; Sequence 73, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; DESCRIPTION: esterase D gene (Accession # M13450)
; DESCRIPTION: nucleotides 777 to 787
; HYPOTHETICAL: NO
```

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; ANTI-SENSE: No
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: chromosome 13
; MAP POSITION: 13q14.1-q14.2
; PUBLICATION INFORMATION:
; AUTHORS: Lee, E Y H P, Lee, W H.
; TITLE: Molecular cloning of the
; TITLE: human esterase D gene, a genetic marker of
; TITLE: retinoblastoma
; JOURNAL: Proceedings of the National Academy of
; JOURNAL: Sciences, USA
; VOLUME: 83
; PAGES: 6337-6341
; DATE: 1986
; RELEVANT RESIDUES IN SEQ ID NO: 73 :FROM 1 TO 11
; US-08-173-489C-73

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAGAAA 627
DB 2 GAAAGAGAAA 10
|||||

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; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis B virus
; INDIVIDUAL ISOLATE: ayw
; PUBLICATION INFORMATION:
; AUTHORS: Galibert, F, Mandart, E, Fitoussi, F,
; AUTHORS: Tiollais, P, Charnay, P.
; TITLE: Nucleotide sequence of the
; TITLE: Hepatitis B virus genome (subtype ayw) cloned
; TITLE: in E coli
; JOURNAL: Nature
; VOLUME: 281
; PAGES: 646-650
; DATE: 1979
; RELEVANT RESIDUES IN SEQ ID NO: 153 :FROM 1 TO 10
; US-08-173-489C-153

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAGAAA 627
DB 10 GGAAGAGAAA 1
|||||

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RESULT 29
US-08-173-489C-153/c
; Sequence 153, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: hepatitis B virus ayw isolate,
; DESCRIPTION: nucleotides 945 to 954

```

```

RESULT 30
US-08-173-489C-203
; Sequence 203, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 203:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: hepatitis B virus adr isolate,
; DESCRIPTION: nucleotides 2103 to 2112
; HYPOTHETICAL: no

```

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; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis B virus
; INDIVIDUAL ISOLATE: adr
; PUBLICATION INFORMATION:
; AUTHORS: Fujiyama, A., Miyanochara, A., No. 5861244aki, C,
; Toneyama, T., Ohromo, N., Matsubara, K.
; TITLE: Cloning and structural
; JOURNAL: analysis of Hepatitis B virus DNAs subtype adr
; VOLUME: 11
; PAGES: 4601-4610
; DATE: 1983
; RELEVANT RESIDUES IN SEQ ID NO: 203 :FROM 1 TO 10
US-08-173-489C-203

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 618 GGAAGAGCTG 627
Db 1 GGAAGAGCTG 10

RESULT 31
US-09-508-753B-48
; Sequence 48, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHAKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 48
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-48

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 624 GAAAGTCTG 633
Db 1 GAAAGAGCTG 10

RESULT 32
US-09-508-753B-71/c
; Sequence 71, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHAKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
```

```
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 71
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-71

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 624 GAAAGTCTG 633
Db 1 GAAAGAGCTG 10

RESULT 33
US-09-769-482-17
; Sequence 17, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: POYNUCLEOTIDE ARRAY
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-769-482-17

Query Match      42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 619 GAAAGAGCTG 628
Db 1 GAAAGAGCTG 10

RESULT 34
5422251-4
; Patent No. 5422251
; APPLICANT: FRESCO, JACQUES R.
; TITLE OF INVENTION: TRIPLE-STRANDED NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,890
; FILING DATE: 28-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 841,218
; FILING DATE: 27-FEB-1992
; APPLICATION NUMBER: 622,330
```

```

;
; FILING DATE: 27-NOV-1990
; APPLICATION NUMBER: 366,244
; FILING DATE: 09-JUN-1989
; APPLICATION NUMBER: 935,047
; FILING DATE: 26-NOV-1986
; SEQ ID NO:4
; LENGTH: 10
5422251-4

Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
DB 1 GGAAGAAAG 10

RESULT 35
5422251-4
; Patent No. 5422251
; APPLICANT: FRESCO, JACQUES R.
; TITLE OF INVENTION: TRIPLE-STRANDED NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,890
; FILING DATE: 28-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 841,218
; FILING DATE: 27-FEB-1992
; APPLICATION NUMBER: 622,330
; FILING DATE: 27-NOV-1990
; APPLICATION NUMBER: 366,244
; FILING DATE: 09-JUN-1989
; APPLICATION NUMBER: 935,047
; FILING DATE: 26-NOV-1986
; SEQ ID NO:4
; LENGTH: 10
5422251-4

Query Match
Best Local Similarity 42.0%; Score 8.4; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
DB 1 GGAAGAAAG 10

RESULT 36
US-08-737-371A-16/c
; Sequence 16, Application US/08737371A
; Patent No. 5959094
; GENERAL INFORMATION:
; APPLICANT: David WALLACH
; APPLICANT: Peter KUHNERT
; APPLICANT: Gotz EHRHARDT
; APPLICANT: Oliver KEMPER
; TITLE OF INVENTION: P/5 TNF RECEPTOR PROMOTERS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,371A
; FILING DATE: 08-NOVEMBER-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05853
; FILING DATE: 11-MAY-1995
; FILING APPLICATION DATA:
; APPLICATION NUMBER: IL 109,633
; FILING DATE: 11-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 17:

```

```

;
; APPLICATION NUMBER: US/08/737,371A
; FILING DATE: 08-NOVEMBER-1996
; PRIOR APPLICATION DATA: PCT/US95/05853
; APPLICATION NUMBER:
; FILING DATE: 11-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109,633
; FILING DATE: 11-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-737-371A-16

Query Match
Best Local Similarity 41.0%; Score 8.2; DB 1; Length 10;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
DB 10 GGAAGAAAG 1

RESULT 37
US-08-737-371A-17
; Sequence 17, Application US/08737371A
; Patent No. 5959094
; GENERAL INFORMATION:
; APPLICANT: David WALLACH
; APPLICANT: Peter KUHNERT
; APPLICANT: Gotz EHRHARDT
; APPLICANT: Oliver KEMPER
; TITLE OF INVENTION: P/5 TNF RECEPTOR PROMOTERS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,371A
; FILING DATE: 08-NOVEMBER-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05853
; FILING DATE: 11-MAY-1995
; FILING APPLICATION DATA:
; APPLICATION NUMBER: IL 109,633
; FILING DATE: 11-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 17:

```

RESULT 39
PCT-US95-05853-17
; Sequence 17, Application PC/TU9505853
; GENERAL INFORMATION:
; APPLICANT:

```

; TITLE OF INVENTION: p75 TNF RECEPTOR PROMOTERS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05853
; FILING DATE: 11-WAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109,633
; FILING DATE: 11-WAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-14 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US95-05853-17

      QY      619 GAAAGAGAAG 628
           |:| ||||:
      Db      1 GRAANGAAS 10

RESULT 40
US-08-662-963-17/c
Sequence 17, Application US/08662963
Patent No. 5738993
GENERAL INFORMATION:
APPLICANT: Mitsubishi Chemical Corporation
TITLE OF INVENTION: Oligonucleotide and Method
of Invention: Analyzing Base Sequence of
Patent No. 5738993
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., Suite 700
CITY: Washington, D.C.
STATE:
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,963
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

```

APPLICANT: Egholm, Michael
APPLICANT: Berg, Rolf H.
APPLICANT: Mollegaard, Neils E.
TITLE OF INVENTION: Higher Order Structure And Binding Of Peptide Nucleic Acids
FILE REFERENCE: IS184290
CURRENT APPLICATION NUMBER: US/09/442,054A
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 08/471,907
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-04-26
PRIOR APPLICATION NUMBER: PCT/ EP92/01219
PRIOR FILING DATE: 1992-05-19
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 78
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. 6770738el Sequence
US-09-442-054A-78

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
DB 1 AAAAGAAA 8

RESULT 43
US-09-442-054A-86/c
Sequence 86, Application US/09442054A
Patent No. 6770738
GENERAL INFORMATION:
APPLICANT: Ecker, David J.
APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Berg, Rolf H.
APPLICANT: Mollegaard, Neils E.
TITLE OF INVENTION: Higher Order Structure And Binding Of Peptide Nucleic Acids
FILE REFERENCE: IS184290
CURRENT APPLICATION NUMBER: US/09/442,054A
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 08/471,907
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-04-26
PRIOR APPLICATION NUMBER: PCT/ EP92/01219
PRIOR FILING DATE: 1992-05-19
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 86
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. 6770738el Sequence
US-09-442-054A-86

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
DB 9 AAAAGAAA 2

RESULT 44
US-08-088-658-4

APPLICANT: Egholm, Michael
APPLICANT: Berg, Rolf H.
APPLICANT: Mollegaard, Neils E.
TITLE OF INVENTION: Higher Order Structure And Binding Of Peptide Nucleic Acids
FILE REFERENCE: IS184290
CURRENT APPLICATION NUMBER: US/09/442,054A
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 08/471,907
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-04-26
PRIOR APPLICATION NUMBER: PCT/ EP92/01219
PRIOR FILING DATE: 1992-05-19
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. 6770738el Sequence
US-09-442-054A-67

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
DB 1 AAAAGAAA 8

RESULT 42
US-09-442-054A-78
Sequence 78, Application US/09442054A
Patent No. 6770738
GENERAL INFORMATION:
APPLICANT: Ecker, David J.
APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Berg, Rolf H.
APPLICANT: Mollegaard, Neils E.
TITLE OF INVENTION: Higher Order Structure And Binding Of Peptide Nucleic Acids
FILE REFERENCE: IS184290
CURRENT APPLICATION NUMBER: US/09/442,054A
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 08/471,907
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-04-26
PRIOR APPLICATION NUMBER: PCT/ EP92/01219
PRIOR FILING DATE: 1992-05-19
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. 6770738el Sequence
US-09-442-054A-67

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
DB 1 AAAAGAAA 8

RESULT 41
US-09-442-054A-67
Sequence 67, Application US/09442054A
Patent No. 6770738
GENERAL INFORMATION:
APPLICANT: Ecker, David J.
APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Berg, Rolf H.
APPLICANT: Mollegaard, Neils E.
TITLE OF INVENTION: Higher Order Structure And Binding Of Peptide Nucleic Acids
FILE REFERENCE: IS184290
CURRENT APPLICATION NUMBER: US/09/442,054A
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 08/471,907
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-04-26
PRIOR APPLICATION NUMBER: PCT/ EP92/01219
PRIOR FILING DATE: 1992-05-19
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. 6770738el Sequence
US-09-442-054A-67

Query Match 40.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 GGAAGAGA 625
DB 8 GGAAGAGA 1

US-08-662-963-17

; Sequence 4, Application US/08088658
; Patent No. 5641625
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; APPLICANT: M llaegaard, Niels E.
; TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/088,658
; FILING DATE: 19930702
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/054,363
; FILING DATE: 26-APRIL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lucci, Joseph
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-088-658-4

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 45
US-08-088-658-43
; Sequence 43, Application US/08088658
; Patent No. 5641625
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; APPLICANT: M llaegaard, Niels E.
; TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia

; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/088,658
; FILING DATE: 19930702
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/054,363
; FILING DATE: 26-APRIL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lucci, Joseph
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-1052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-088-658-43

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 46
US-08-686-116A-49
; Sequence 49, Application US/08686116A
; Patent No. 5714331
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Binding Affinity, Sequence Specificity
; Patent No. 5714331
; TITLE OF INVENTION: ans Solubility
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5714331ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/686,116A
; FILING DATE: July 24, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2271

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-686-116A-49

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 47
US-08-686-116A-51
Sequence 51, Application US/08686116A
Patent No. 5714331
GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
TITLE OF INVENTION: Binding Affinity, Sequence Specificity
Patent No. 5714331
TITLE OF INVENTION: ans Solubility
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5714331rlis LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,116A
FILING DATE: July 24, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-2271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-686-116A-51

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 48
US-08-685-484-49
Sequence 49, Application US/08685484
Patent No. 5719262
GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
TITLE OF INVENTION: Side Chains
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5719262rlis LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,484
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-2270
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-685-484-49

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 49
US-08-685-484-51
Sequence 51, Application US/08685484
Patent No. 5719262
GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
TITLE OF INVENTION: Side Chains
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5719262rlis LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,484
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-2270
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-685-484-49

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 49
US-08-685-484-51
Sequence 51, Application US/08685484
Patent No. 5719262
GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
TITLE OF INVENTION: Side Chains
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5719262rlis LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

```

; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,484
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-685-484-51

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 50
US-08-847-108-49
; Sequence 49, Application US/08847108
; Patent No. 5736336
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Binding Affinity, Sequence Specificity
; Patent No. 5736336
; TITLE OF INVENTION: and Solubility
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736336ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,108
; FILING DATE: 01-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,116
; FILING DATE: July 24, 1996
; REFERENCE/DOCKET NUMBER: ISIS-2271
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,108
; FILING DATE: 01-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,116
; FILING DATE: July 24, 1996
; REFERENCE/DOCKET NUMBER: ISIS-2271
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-847-108-51

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 52
US-08-686-113A-56
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```

; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-847-108-49

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 51
US-08-847-108-51
; Sequence 51, Application US/08847108
; Patent No. 5736336
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Binding Affinity, Sequence Specificity
; Patent No. 5736336
; TITLE OF INVENTION: and Solubility
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736336ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,108
; FILING DATE: 01-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,116
; FILING DATE: July 24, 1996
; REFERENCE/DOCKET NUMBER: ISIS-2271
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-847-108-51

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 52
US-08-686-113A-56
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usl0619220-65.rni.sl

Fri Apr 15 13:23:04 2005

```
; Sequence 56, Application US/08686113A
; Patent No. 5766855
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Affinity And Sequence Specificity
; Patent No. 5766855
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5766855ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/686,113A
; FILING DATE: July 24, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2273
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-686-113A-56

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 53
US-08-686-113A-58
; Sequence 58, Application US/08686113A
; Patent No. 5766855
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Affinity And Sequence Specificity
; Patent No. 5766855
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5766855ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/686,113A
; FILING DATE: July 24, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2273
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-686-113A-58

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 54
US-08-847-095A-49
; Sequence 49, Application US/08847095A
; Patent No. 5786461
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
; TITLE OF INVENTION: Side Chains
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5786461ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,095A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,484
; FILING DATE: 24-JUL-1996
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2270
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/686,113A
; FILING DATE: July 24, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2273
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-686-113A-58

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 54
US-08-847-095A-49
; Sequence 49, Application US/08847095A
; Patent No. 5786461
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
; TITLE OF INVENTION: Side Chains
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5786461ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,095A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,484
; FILING DATE: 24-JUL-1996
; APPLICATION NUMBER: 08/108,591
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael P. Straher
; REGISTRATION NUMBER: 38,325
; REFERENCE/DOCKET NUMBER: ISIS-2270
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
US-08-847-095A-49

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
DB 2 AAAAGAAA 9

RESULT 55

US-08-847-095A-51
; Sequence 51, Application US/08847095A
; Patent No. 5786461
; GENERAL INFORMATION:
; APPLICANT: Buchardt et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
; TITLE OF INVENTION: Side Chains
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5786461Iris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847, 095A
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,484
FILING DATE: 24-JUL-1996
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-2270
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-847-095A-51

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
DB 1 AAAAGAAA 8

RESULT 56

US-08-471-907A-4
; Sequence 4, Application US/08471907A
; Patent No. 5986053
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole

; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; APPLICANT: M lilegaard, Niels E.
; TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053Iris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,907A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/088,658
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-1052
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-471-907A-4

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
DB 2 AAAAGAAA 9

RESULT 57

US-08-471-907A-43
; Sequence 43, Application US/08471907A
; Patent No. 5986053
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole

; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; APPLICANT: M lilegaard, Niels E.
; TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053Iris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Deacon, Nicholas J.
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/088,658
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-1052
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-907A-43

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
|||||
DB 1 AAAAGAAA 8

RESULT 58
US-08-388-353-272
Sequence 272, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 272:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-272

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
|||||
DB 3 AAAAGAAA 10

RESULT 59
US-08-388-353-273
Sequence 273, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-273

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
|||||
DB 2 AAAAGAAA 9

RESULT 60
US-08-388-353-274
Sequence 274, Application US/08388353
Patent No. 6010895

```

; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 274:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-274

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8
|||||

RESULT 61
US-08-488-551B-272
; Sequence 272, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995

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; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-272

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 3 AAAAGAAA 10
|||||

RESULT 62
US-08-488-551B-273
; Sequence 273, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995

```

ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGILIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-273

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 63
US-08-488-551B-274
Sequence 274, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Date A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGILIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 274:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-488-551B-274
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 64
US-08-857-721-1
Sequence 1, Application US/08857721B
Patent No. 6218108
GENERAL INFORMATION:
APPLICANT: Kool, Eric
TITLE OF INVENTION: NOVEL NUCLEOTIDE ANALOGS WITH POLYCYCLIC AROMATIC
FILE OF INVENTION: GROUPS ATTACHED, METHODS OF SYNTHESIS AND USES THEREFOR
FILE REFERENCE: Research
CURRENT APPLICATION NUMBER: US/08/857,721B
CURRENT FILING DATE: 1997-05-15
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetically
OTHER INFORMATION: generated DNA oligonucleotide
US-08-857-721-1

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAAA 626
Db 1 GAAAGAAA 8

RESULT 65
US-08-088-661F-20
Sequence 20, Application US/08088661F
Patent No. 6228982
GENERAL INFORMATION:
APPLICANT: No. 6228982den, Benget
APPLICANT: Wittung, Pernilla
APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Nielsen, Peter E.
APPLICANT: Berg, Rolf
TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids
FILE REFERENCE: ISIS1108
CURRENT APPLICATION NUMBER: US/08/088,661F
CURRENT FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-04-26
PRIOR APPLICATION NUMBER: PCT/EP92/01219
PRIOR FILING DATE: 1992-05-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence
US-08-088-661F-20

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
|||||
Db 2 AAAAGAAA 9

RESULT 66

US-08-088-661P-22
; Sequence 22, Application US/08088661P
; Patent No. 6228982
; GENERAL INFORMATION:
; APPLICANT: No. 6228982den, Bengel
; APPLICANT: Wittung, Pernilla
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf
; TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids
; FILE REFERENCE: ISIS1108
; CURRENT APPLICATION NUMBER: US/08/088,661P
; CURRENT FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 08/054,363
; PRIOR FILING DATE: 1993-04-26
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence
US-08-088-661P-22

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
|||||
Db 1 AAAAGAAA 8

RESULT 67

US-08-899-241-241/c
; Sequence 241, Application US/08899241A
; Patent No. 6322995
; GENERAL INFORMATION:
; APPLICANT: Hohmann, Hans-Peter
; APPLICANT: Huemelin, Markus
; APPLICANT: van Loon, Adolphus
; APPLICANT: Schurter, Walter
; TITLE OF INVENTION: Improved Riboflavin Production
; FILE REFERENCE: Improved Riboflavin Prod
; CURRENT APPLICATION NUMBER: US/08/899,241A
; CURRENT FILING DATE: 1997-07-23
; EARLIER APPLICATION NUMBER: 96111905.4
; EARLIER FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 241
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Ac# X02730
US-08-899-241-241

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 622 AAGAAAGT 629

Db 8 AAGAAAGT 1
|||||

RESULT 68

US-08-150-156A-2
; Sequence 2, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150,156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-08-150-156A-2

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
|||||
Db 1 AAAAGAAA 8

RESULT 69

US-08-150-156A-5
; Sequence 5, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150,156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DK 0987/91
;; FILING DATE: 24-MAY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DK 0510/92
;; FILING DATE: 15-APR-1992
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; PUBLICATION INFORMATION:
;; DOCUMENT NUMBER: WO PCT/EP92/01220
;; FILING DATE: 22-MAY-1992
;; US-08-150-156A-5

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
|||
Db 2 AAAAGAAA 9

RESULT 70
US-08-150-156A-14/c
; Sequence 14, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150,156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
; US-08-150-156A-14

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
|||
Db 9 AAAAGAAA 2

RESULT 71
US-08-150-156A-16/c
; Sequence 16, Application US/08150156A
; Patent No. 6357163
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
; DIAGNOSTICS AND ANALYTICAL PROCEDURES
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150,156A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0986/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0987/91
; FILING DATE: 24-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0510/92
; FILING DATE: 15-APR-1992
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
; US-08-150-156A-16

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
|||
Db 10 AAAAGAAA 3

RESULT 72
US-08-108-591B-8
; Sequence 8, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-8

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      620 AAAAGAAA 627
DB      2 AAAAGAAA 9

RESULT 73
US-08-108-591B-9
; Sequence 9, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-9

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      620 AAAAGAAA 627
DB      2 AAAAGAAA 9

RESULT 74
US-08-108-591B-10
; Sequence 10, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-10

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      620 AAAAGAAA 627
DB      2 AAAAGAAA 9

RESULT 75
US-08-108-591B-12/c
; Sequence 12, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-12

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      620 AAAAGAAA 627
DB      9 AAAAGAAA 2

RESULT 76
US-08-108-591B-14/c
; Sequence 14, Application US/08108591B
; Patent No. 6395474
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS0540
; CURRENT APPLICATION NUMBER: US/08/108,591B
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-14

Query Match      40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      620 AAAAGAAA 627
DB      10 AAAAGAAA 3

RESULT 77
US-08-686-114B-56
; Sequence 56, Application US/08686114B
; Patent No. 6414112
; GENERAL INFORMATION:
```

APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleob
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6414112ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,114B
FILING DATE: July 24, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-2272
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-686-114B-56

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 78
US-08-686-114B-58
Sequence 58, Application US/08686114B
Patent No. 6414112
GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleob
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6414112ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,114B
FILING DATE: July 24, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-2272
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-686-114B-58

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 79
US-09-475-947A-80/c
Sequence 80, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 80
LENGTH: 10
TYPE: DNA
ORGANISM: human
US-09-475-947A-80

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 AAAAGAAAG 628
Db 9 AAAAGAAAG 2

RESULT 80
US-09-475-947A-142
Sequence 142, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 142
LENGTH: 10
TYPE: DNA
ORGANISM: human
US-09-475-947A-142

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 AAGAAAG 628
Db 3 AAGAAAG 10
|||||

RESULT 81

US-09-508-753B-140
; Sequence 140, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiichi OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 140
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-140

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 CGGAAAG 624
Db 1 CGGAAAG 8
|||||

RESULT 82

US-09-508-753B-208/c
; Sequence 208, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiichi OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 208
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-208

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 CGGAAAG 624
Db 10 CGGAAAG 3
|||||

RESULT 83

US-09-337-304-56
; Sequence 56, Application US/09337304
; Patent No. 6613873
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2, 6-Diaminopurine Nucleobases
; FILE REFERENCE: ISIS-3809
; CURRENT APPLICATION NUMBER: US/09/337,304
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 08/847,110
; PRIOR FILING DATE: 1997-05-01
; PRIOR APPLICATION NUMBER: 08/686,114
; PRIOR FILING DATE: 1996-07-24
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 986/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 510/92
; PRIOR FILING DATE: 1992-04-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 56
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-337-304-56

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAA 627
Db 2 AAAAGAA 9
|||||

RESULT 84

US-09-337-304-58
; Sequence 58, Application US/09337304
; Patent No. 6613873
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2, 6-Diaminopurine Nucleobases
; FILE REFERENCE: ISIS-3809
; CURRENT APPLICATION NUMBER: US/09/337,304
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 08/847,110
; PRIOR FILING DATE: 1997-05-01
; PRIOR APPLICATION NUMBER: 08/686,114
; PRIOR FILING DATE: 1996-07-24
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 986/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 987/91
; PRIOR FILING DATE: 1991-05-24

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; PRIOR APPLICATION NUMBER: 510/92
; PRIOR FILING DATE: 1992-04-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-337-304-58

Query Match          40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 85
US-08-468-719A-8
; Sequence 8, Application US/08468719A
; Patent No. 6710163
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS SYNTHONS
; FILE REFERENCE: ISPS-1999
; CURRENT APPLICATION NUMBER: US/08/468,719A
; CURRENT FILING DATE: 1995-06-06
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-08-468-719A-8

Query Match          40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 86
US-08-468-719A-10
; Sequence 10, Application US/08468719A
; Patent No. 6710163
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS SYNTHONS
; FILE REFERENCE: ISPS-1999
; CURRENT APPLICATION NUMBER: US/08/468,719A
; CURRENT FILING DATE: 1995-06-06
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10

; PRIOR APPLICATION NUMBER: 510/92
; PRIOR FILING DATE: 1992-04-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-337-304-58

Query Match          40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 87
US-08-468-719A-12/c
; Sequence 12, Application US/08468719A
; Patent No. 6710163
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS SYNTHONS
; FILE REFERENCE: ISPS-1999
; CURRENT APPLICATION NUMBER: US/08/468,719A
; CURRENT FILING DATE: 1995-06-06
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-08-468-719A-12

Query Match          40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 9 AAAAGAAA 2

RESULT 88
US-08-468-719A-14/c
; Sequence 14, Application US/08468719A
; Patent No. 6710163
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.
; TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS SYNTHONS
; FILE REFERENCE: ISPS-1999
; CURRENT APPLICATION NUMBER: US/08/468,719A
; CURRENT FILING DATE: 1995-06-06
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
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US-08-468-719A-14

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 10 AAAAGAAA 3
|||||

RESULT 89

US-08-468-719A-46/c
; Sequence 46, Application US/08468719A
; Patent No. 6710163
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Berg, Rolf H.

; TITLE OF INVENTION: PEPTIDE NUCLEIC ACIDS SYNTHONS
; FILE REFERENCE: ISPS-1999
; CURRENT APPLICATION NUMBER: US/08/468,719A
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/108,591
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 10
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-08-468-719A-46

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 10 AAAAGAAA 3
|||||

RESULT 90

US-09-230-088-49
; Sequence 49, Application US/09230088
; Patent No. 6710164
; GENERAL INFORMATION:

; APPLICANT: Nielsen, Peter
; APPLICANT: Egholm, Michael
; APPLICANT: Berg, Rolf
; APPLICANT: Buchardt, Ole
; APPLICANT: Buchardt, Dorte
; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced Binding Affinity, Sequence
; FILE REFERENCE: ISIS2535
; CURRENT APPLICATION NUMBER: US/09/230,088

; CURRENT FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: PCT/US97/12811
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: 08/685,484
; PRIOR FILING DATE: 1996-07-24
; PRIOR APPLICATION NUMBER: 08/686,116
; PRIOR FILING DATE: 1996-07-24
; PRIOR APPLICATION NUMBER: 08/686,114
; PRIOR FILING DATE: 1996-07-24
; PRIOR APPLICATION NUMBER: 08/686,113
; PRIOR FILING DATE: 1996-07-24
; PRIOR APPLICATION NUMBER: 60/051,002
; PRIOR FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: 08/108,591

; PRIOR FILING DATE: 1993-11-22

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 49

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: No. 6710164el Sequence

US-09-230-088-49

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9
|||||

RESULT 91

US-09-230-088-51

; Sequence 51, Application US/09230088

; Patent No. 6710164

; GENERAL INFORMATION:

; APPLICANT: Nielsen, Peter

; APPLICANT: Egholm, Michael

; APPLICANT: Berg, Rolf

; APPLICANT: Buchardt, Ole

; APPLICANT: Buchardt, Dorte

; TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced Binding Affinity, Sequence
; FILE REFERENCE: ISIS2535
; CURRENT APPLICATION NUMBER: US/09/230,088

; CURRENT FILING DATE: 1999-03-10

; PRIOR APPLICATION NUMBER: PCT/US97/12811

; PRIOR FILING DATE: 1997-07-24

; PRIOR APPLICATION NUMBER: 08/685,484

; PRIOR FILING DATE: 1996-07-24

; PRIOR APPLICATION NUMBER: 08/686,116

; PRIOR FILING DATE: 1996-07-24

; PRIOR APPLICATION NUMBER: 08/686,114

; PRIOR FILING DATE: 1996-07-24

; PRIOR APPLICATION NUMBER: 08/686,113

; PRIOR FILING DATE: 1997-05-29

; PRIOR APPLICATION NUMBER: 08/108,591

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 51

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: No. 6710164el Sequence

US-09-230-088-51

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8
|||||

RESULT 92

US-08-462-977B-8

; Sequence 8, Application US/08462977B

; Patent No. 6713602
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS-1993
; CURRENT APPLICATION NUMBER: US/08/462,977B
; CURRENT FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: No. 6713602el Sequence
US-08-462-977B-8

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 2 AAAAGAAA 9

RESULT 93
US-08-462-977B-10
; Sequence 10, Application US/08462977B
; Patent No. 6713602
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS-1993
; CURRENT APPLICATION NUMBER: US/08/462,977B
; CURRENT FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: No. 6713602el Sequence
US-08-462-977B-10

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 1 AAAAGAAA 8

RESULT 94
US-08-462-977B-12/c
; Sequence 12, Application US/08462977B
; Patent No. 6713602
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole

; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS-1993
; CURRENT APPLICATION NUMBER: US/08/462,977B
; CURRENT FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: No. 6713602el Sequence
US-08-462-977B-12

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 9 AAAAGAAA 2

RESULT 95
US-08-462-977B-14/c
; Sequence 14, Application US/08462977B
; Patent No. 6713602
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter Eigil
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISIS-1993
; CURRENT APPLICATION NUMBER: US/08/462,977B
; CURRENT FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: No. 6713602el Sequence
US-08-462-977B-14

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
Db 10 AAAAGAAA 3

RESULT 96
US-09-442-054A-43
; Sequence 43, Application US/09442054A
; Patent No. 6770738
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Berg, Rolf H.

; APPLICANT: Mollegaard, Neils E.
 ; TITLE OF INVENTION: Higher Order Structure And Binding Of Peptide Nucleic Acids
 ; FILE REFERENCE: IS154290
 ; CURRENT APPLICATION NUMBER: US/09/442,054A
 ; CURRENT FILING DATE: 2002-05-07
 ; PRIOR APPLICATION NUMBER: 08/471,907
 ; PRIOR FILING DATE: 1995-06-07
 ; PRIOR APPLICATION NUMBER: 08/054,363
 ; PRIOR FILING DATE: 1993-04-26
 ; PRIOR APPLICATION NUMBER: PCT/EP92/01219
 ; PRIOR FILING DATE: 1992-05-19
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 43
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: No. 6770738el Sequence
 US-09-442-054A-43

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
 Db 1 AAAAGAAA 8

RESULT 97
 US-09-442-054A-58
 ; Sequence 58, Application US/09442054A
 ; Patent No. 6770738
 ; GENERAL INFORMATION:
 ; APPLICANT: Ecker, David J.
 ; APPLICANT: Buchardt, Ole
 ; APPLICANT: Egholm, Michael
 ; APPLICANT: Berg, Rolf H.
 ; APPLICANT: Mollegaard, Neils E.
 ; TITLE OF INVENTION: Higher Order Structure And Binding Of Peptide Nucleic Acids
 ; FILE REFERENCE: IS154290
 ; CURRENT APPLICATION NUMBER: US/09/442,054A
 ; CURRENT FILING DATE: 2002-05-07
 ; PRIOR APPLICATION NUMBER: 08/471,907
 ; PRIOR FILING DATE: 1995-06-07
 ; PRIOR APPLICATION NUMBER: 08/054,363
 ; PRIOR FILING DATE: 1993-04-26
 ; PRIOR APPLICATION NUMBER: PCT/EP92/01219
 ; PRIOR FILING DATE: 1992-05-19
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 58
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: No. 6770738el Sequence
 US-09-442-054A-58

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
 Db 2 AAAAGAAA 9

RESULT 98
 US-08-853-980-1/c
 ; Sequence 1, Application US/08853980
 ; Patent No. 6225082

; GENERAL INFORMATION:
 ; APPLICANT: Carson, John H.
 ; APPLICANT: Kwon, Sunjong
 ; APPLICANT: Aigner, Kevin
 ; APPLICANT: Avossa, Daniela
 ; TITLE OF INVENTION: MYELIN BASIC PROTEIN mRNA TRANSPORT AND TRANSLATION
 ; TITLE OF INVENTION: ENHANCER SEQUENCES
 ; FILE REFERENCE: RCT
 ; CURRENT APPLICATION NUMBER: US/08/853,980
 ; CURRENT FILING DATE: 1997-05-09
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 8
 ; TYPE: RNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Myelin Basic
 ; OTHER INFORMATION: protein consensus sequence
 US-08-853-980-1

Query Match 38.0%; Score 7.6; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 2.5e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 621 AAAGAAAG 628
 Db 8 AAAGAAAG 1

RESULT 99
 US-09-375-673B-33
 ; Sequence 33, Application US/09375673B
 ; Patent No. 6605431
 ; GENERAL INFORMATION:
 ; APPLICANT: GOURSE, RICHARD L.
 ; APPLICANT: ESTREM, SHAWN T.
 ; APPLICANT: ROSS, WILLMA E.
 ; APPLICANT: GAAL, TAMAS
 ; TITLE OF INVENTION: PROMOTER ELEMENTS AND METHODS OF USE
 ; FILE REFERENCE: 11900130101
 ; CURRENT APPLICATION NUMBER: US/09/375,673B
 ; CURRENT FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 33
 ; LENGTH: 9
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Proximal
 ; OTHER INFORMATION: accessory promoter element
 US-09-375-673B-33

Query Match 37.0%; Score 7.4; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 622 AAGAAAGTG 630
 Db 1 AAGAAAGTG 9

Search completed: April 15, 2005, 13:04:10
 Job time : 1 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 12:57:15 ; Search time 0.001 Seconds
(without alignments)
105.760 Million cell updates/sec

Title: US-10-619-220-65

Perfect score: 20

Sequence: 1 ccggaagaagaagtgcgga 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 241 seqs, 2644 residues

Total number of hits satisfying chosen parameters: 482

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 241 summaries

Database : usl0619220-65.rng.subdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	20	100.0	20	1	Antisense oligonuc
C 2	20	100.0	20	1	Mouse Fas chimeric
C 3	20	100.0	20	1	Antisense oligonuc
C 4	20	100.0	20	1	Labelled ISIS 2202
C 5	20	100.0	20	1	Mouse Fas cDNA, an
C 6	20	100.0	20	1	Mouse Fas antisens
C 7	20	100.0	20	1	Fatty acid synthas
C 8	20	100.0	20	1	Fas antisense olig
C 9	12.4	62.0	15	1	Human IL-5 hammerh
C 10	12.4	62.0	15	1	Human IL-5 hammerh
C 11	11.4	57.0	13	1	CFTR gene associat
C 12	11.4	57.0	13	1	DNA array associat
C 13	11	55.0	12	1	Oligonucleotide pr
C 14	11	55.0	13	1	Oligonucleotide SE
C 15	11	55.0	13	1	Oligonucleotide SE
C 16	11	55.0	13	1	Oligonucleotide SE
C 17	11	55.0	13	1	Oligonucleotide pr
C 18	10.4	52.0	12	1	Oligonucleotide pr
C 19	10.4	52.0	12	1	Oligonucleotide pr
C 20	10.4	52.0	13	1	Oligonucleotide SE
C 21	10.4	52.0	13	1	Oligonucleotide SE
C 22	10.4	52.0	13	1	Oligonucleotide SE
C 23	10.4	52.0	13	1	Oligonucleotide SE
C 24	10.4	52.0	13	1	Oligonucleotide SE
C 25	10.4	52.0	13	1	Oligonucleotide SE
C 26	10.4	52.0	13	1	Oligonucleotide SE
C 27	10.4	52.0	13	1	Oligonucleotide SE
C 28	10.4	52.0	13	1	Oligonucleotide SE
C 29	10.4	52.0	13	1	Oligonucleotide SE
C 30	10.4	52.0	13	1	Oligonucleotide SE
C 31	10.4	52.0	13	1	Oligonucleotide SE
C 32	10.4	52.0	13	1	Oligonucleotide SE
C 33	10.4	52.0	13	1	Oligonucleotide SE

C 34	10.4	52.0	13	1	ABH62583	Oligonucleotide SE
C 35	10.4	52.0	13	1	ABH60876	Oligonucleotide SE
C 36	10.4	52.0	13	1	ABF91393	Oligonucleotide SE
C 37	10	50.0	11	1	AAAS4622	Endothelial moocy
C 38	10	50.0	11	1	AAA34069	Human adenosine re
C 39	10	50.0	11	1	AAF20191	Human endothelial
C 40	10	50.0	11	1	ABQ86415	Human skin stress/
C 41	10	50.0	11	1	ABQ86415	Human skin stress/
C 42	10	50.0	11	1	ABQ86415	Human skin stress/
C 43	10	50.0	11	1	ABQ86415	Human skin stress/
C 44	10	50.0	11	1	ABQ86415	Human skin stress/
C 45	10	50.0	11	1	ABQ86415	Human skin stress/
C 46	10	50.0	11	1	ABQ86415	Human skin stress/
C 47	10	50.0	11	1	ABQ86415	Human skin stress/
C 48	10	50.0	11	1	ABQ86415	Human skin stress/
C 49	10	50.0	11	1	ABQ86415	Human skin stress/
C 50	10	50.0	11	1	ABQ86415	Human skin stress/
C 51	10	50.0	11	1	ABQ86415	Human skin stress/
C 52	10	50.0	11	1	ABQ86415	Human skin stress/
C 53	10	50.0	11	1	ABQ86415	Human skin stress/
C 54	10	50.0	11	1	ABQ86415	Human skin stress/
C 55	10	50.0	11	1	ABQ86415	Human skin stress/
C 56	10	50.0	11	1	ABQ86415	Human skin stress/
C 57	10	50.0	11	1	ABQ86415	Human skin stress/
C 58	10	50.0	11	1	ABQ86415	Human skin stress/
C 59	10	50.0	11	1	ABQ86415	Human skin stress/
C 60	10	50.0	11	1	ABQ86415	Human skin stress/
C 61	10	50.0	11	1	ABQ86415	Human skin stress/
C 62	10	50.0	11	1	ABQ86415	Human skin stress/
C 63	10	50.0	11	1	ABQ86415	Human skin stress/
C 64	10	50.0	11	1	ABQ86415	Human skin stress/
C 65	10	50.0	11	1	ABQ86415	Human skin stress/
C 66	10	50.0	11	1	ABQ86415	Human skin stress/
C 67	10	50.0	11	1	ABQ86415	Human skin stress/
C 68	10	50.0	11	1	ABQ86415	Human skin stress/
C 69	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 70	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 71	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 72	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 73	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 74	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 75	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 76	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 77	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 78	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 79	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 80	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 81	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 82	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 83	9.4	47.0	11	1	ABQ86415	Human skin stress/
C 84	9	45.0	10	1	AAAS1980	Metastatic breast
C 85	9	45.0	10	1	AAAS1980	Prokaryote RT-PCR
C 86	9	45.0	10	1	AAAS1980	Human interleukin
C 87	9	45.0	10	1	AAAS1980	Human interleukin
C 88	9	45.0	10	1	AAAS1980	Primer for detecti
C 89	9	45.0	10	1	AAAS1980	Yeast NORF gene SA
C 90	9	45.0	10	1	AAAS1980	Yeast NORF gene SA
C 91	9	45.0	10	1	AAAS1980	Yeast NORF gene SA
C 92	9	45.0	10	1	AAAS1980	Yeast NORF gene SA
C 93	9	45.0	10	1	AAAS1980	Primer #6 to detec
C 94	9	45.0	10	1	AAAS1980	Human ICAM2 gene a
C 95	9	45.0	10	1	AAAS1980	Human interleukin
C 96	9	45.0	10	1	AAAS1980	Human interleukin
C 97	9	45.0	10	1	AAAS1980	Human IL8B gene a
C 98	9	45.0	10	1	AAAS1980	EST polymorphic DN
C 99	9	45.0	10	1	AAAS1980	EST polymorphic DN
C 100	9	45.0	10	1	AAAS1980	Zinc finger protei
C 101	9	45.0	10	1	AAAS1980	Triple helix formi
C 102	9	45.0	10	1	AAAS1980	Human skin stress/
C 103	9	45.0	10	1	AAAS1980	Human skin stress/
C 104	9	45.0	10	1	AAAS1980	Human skin stress/
C 105	9	45.0	10	1	AAAS1980	Human skin stress/
C 106	9	45.0	10	1	AAAS1980	Human skin stress/

107	9	45.0	11	1	AD026297	Human chondromedin	180	8	40.0	10	1	AAQ81102	Peptide nucleic ac
108	9	45.0	11	1	ADQ33318	Human facial skin-	c 181	8	40.0	10	1	AAQ81121	Peptide nucleic ac
109	8.4	42.0	10	1	AA114816	Triple helix formi	182	8	40.0	10	1	AAQ96677	HIV-1 NL4-3 nef ge
c 110	8.4	42.0	10	1	AA114766	Triple helix formi	183	8	40.0	10	1	AAQ96678	HIV-1 NL4-3 nef ge
c 111	8.4	42.0	10	1	AA020953	WO9504041 Seq ID 6	184	8	40.0	10	1	AAQ96676	HIV-1 NL4-3 nef ge
c 112	8.4	42.0	10	1	AAZ77678	Human dendritic ce	185	8	40.0	10	1	AAV50338	Yeast tag for addi
c 113	8.4	42.0	10	1	AAZ78980	Human dendritic ce	186	8	40.0	10	1	AAV11235	Seq ID #51 from WO
c 114	8.4	42.0	10	1	AAZ78664	Human dendritic ce	187	8	40.0	10	1	AAV11233	Seq ID #49 from WO
c 115	8.4	42.0	10	1	AAZ78219	Human dendritic ce	188	8	40.0	10	1	AAZ78164	Human dendritic ce
c 116	8.4	42.0	10	1	AAZ83766	Metastatic breast	189	8	40.0	10	1	AAZ78206	Human dendritic ce
c 117	8.4	42.0	10	1	AAZ83450	Metastatic breast	c 190	8	40.0	10	1	AAZ85759	Metastatic breast
c 118	8.4	42.0	10	1	AAZ81243	Metastatic breast	191	8	40.0	10	1	AAZ85029	Metastatic breast
c 119	8.4	42.0	10	1	AAZ81950	Metastatic breast	192	8	40.0	10	1	AAZ82002	Metastatic breast
c 120	8.4	42.0	10	1	AAZ83641	Metastatic breast	c 193	8	40.0	10	1	AAZ84727	Metastatic breast
c 121	8.4	42.0	10	1	AAZ83175	Metastatic breast	194	8	40.0	10	1	AAZ82056	Metastatic breast
c 122	8.4	42.0	10	1	AAZ81051	Metastatic breast	c 195	8	40.0	10	1	AAZ84801	Metastatic breast
c 123	8.4	42.0	10	1	AAZ84388	Metastatic breast	c 196	8	40.0	10	1	AAZ84861	Metastatic breast
c 124	8.4	42.0	10	1	AAZ85130	Metastatic breast	197	8	40.0	10	1	AAZ83013	Metastatic breast
c 125	8.4	42.0	10	1	AAZ81581	Metastatic breast	c 198	8	40.0	10	1	AAZ81715	Metastatic breast
c 126	8.4	42.0	10	1	AAZ74107	Human dendritic ce	199	8	40.0	10	1	AAZ85291	Metastatic breast
c 127	8.4	42.0	10	1	AAA56494	Human macrophage g	200	8	40.0	10	1	AAH63545	Human ubiquitously
c 128	8.4	42.0	10	1	AAA56419	Human macrophage g	201	8	40.0	10	1	AAH63707	Human ubiquitously
c 129	8.4	42.0	10	1	AAH63756	Human ubiquitously	202	8	40.0	10	1	AAH64124	Human ubiquitously
c 130	8.4	42.0	10	1	AAH64268	Human ubiquitously	c 203	8	40.0	10	1	AAF81044	Primer for detecti
c 131	8.4	42.0	10	1	AAH63755	Human ubiquitously	204	8	40.0	10	1	AAF36878	Yeast NORF gene SA
c 132	8.4	42.0	10	1	AAF98126	Human IGERA gene p	c 205	8	40.0	10	1	AAF39485	Yeast NORF gene SA
c 133	8.4	42.0	10	1	AAH32738	LPS activated huma	c 206	8	40.0	10	1	AAF36657	Yeast NORF gene SA
c 134	8.4	42.0	10	1	AAF33775	Yeast NORF gene SA	207	8	40.0	10	1	AAF37047	Yeast NORF gene SA
c 135	8.4	42.0	10	1	AAF33616	Yeast NORF gene SA	c 208	8	40.0	10	1	AAF36327	Yeast NORF gene SA
c 136	8.4	42.0	10	1	AAF34158	Yeast NORF gene SA	209	8	40.0	10	1	AAF36916	Yeast NORF gene SA
c 137	8.4	42.0	10	1	AAF39587	Yeast NORF gene SA	c 210	8	40.0	10	1	AAF42384	Yeast NORF gene SA
c 138	8.4	42.0	10	1	AAF36214	Yeast NORF gene SA	211	8	40.0	10	1	AAF42677	Yeast NORF gene SA
c 139	8.4	42.0	10	1	AAF33615	Yeast NORF gene SA	c 212	8	40.0	10	1	AAF41024	Yeast NORF gene SA
c 140	8.4	42.0	10	1	AAF40411	Yeast NORF gene SA	213	8	40.0	10	1	AAF33555	Yeast NORF gene SA
c 141	8.4	42.0	10	1	AAF38491	Yeast NORF gene SA	214	8	40.0	10	1	AAF39862	Yeast NORF gene SA
c 142	8.4	42.0	10	1	AAF35093	Yeast NORF gene SA	215	8	40.0	10	1	AAF36127	Yeast NORF gene SA
c 143	8.4	42.0	10	1	AAF43945	Yeast NORF gene SA	216	8	40.0	10	1	AAF43071	Yeast NORF gene SA
c 144	8.4	42.0	10	1	AAF38986	Yeast NORF gene SA	c 217	8	40.0	10	1	AAF43599	Yeast NORF gene SA
c 145	8.4	42.0	10	1	AAF39649	Yeast NORF gene SA	c 218	8	40.0	10	1	AAF34701	Yeast NORF gene SA
c 146	8.4	42.0	10	1	AAF43948	Yeast NORF gene SA	219	8	40.0	10	1	AAF38720	Yeast NORF gene SA
c 147	8.4	42.0	10	1	AAF34952	Yeast NORF gene SA	c 220	8	40.0	10	1	AAF34650	Yeast NORF gene SA
c 148	8.4	42.0	10	1	AAF38358	Yeast NORF gene SA	c 221	8	40.0	10	1	AAF35643	Yeast NORF gene SA
c 149	8.4	42.0	10	1	AAF41701	Yeast NORF gene SA	222	8	40.0	10	1	AAF38421	Yeast NORF gene SA
c 150	8.4	42.0	10	1	AAF35215	Yeast NORF gene SA	c 223	8	40.0	10	1	AAF43757	Yeast NORF gene SA
c 151	8.4	42.0	10	1	AAF36378	Yeast NORF gene SA	224	8	40.0	10	1	ABK86470	Human apo-dystroph
c 152	8.4	42.0	10	1	ABS64900	Primer-extension o	c 225	8	40.0	10	1	ABK86076	Human apo-dystroph
c 153	8.4	42.0	10	1	ABL42853	Human maturation/a	226	8	40.0	10	1	ABL99008	Mouse neuronal reg
c 154	8.4	42.0	10	1	ABL42926	Human maturation/a	c 227	8	40.0	10	1	ABL7004	Pyridoxal (Pyridox
c 155	8.4	42.0	10	1	ABK81442	SCYA20 primer exte	228	8	40.0	10	1	AAS99195	UDP glycosyltransf
c 156	8.4	42.0	10	1	ABQ72882	Human GRM8 gene po	c 229	8	40.0	10	1	ABV78516	Human Th1 cell pre
c 157	8.4	42.0	10	1	ABL36382	Human lysosomal ac	230	8	40.0	10	1	ABV84212	Human haemoglobin
c 158	8.4	42.0	10	1	ADG28123	Human Myo/Vi prote	231	8	40.0	10	1	ABV84745	Human haemoglobin
c 159	8.4	42.0	10	1	ACA94429	DNA tag from human	c 232	8	40.0	10	1	ABK23615	Transcript tag DNA
c 160	8.4	42.0	10	1	ACC41709	Zinc finger protei	233	8	40.0	10	1	ABK28549	Paraoxonase 2 (PON
c 161	8.4	42.0	10	1	AD601116	Human androgen-reg	c 234	8	40.0	10	1	ABK81797	Human CHRM5 gene p
c 162	8.4	42.0	10	1	ADE14173	Optineurin promote	235	8	40.0	10	1	AAL39786	SMOH polymorphism
c 163	8.4	42.0	10	1	ADG98629	Human CETP gene al	c 236	8	40.0	10	1	ABX79755	EST polymorphic DN
c 164	8.4	42.0	10	1	ADG89969	Human TNFRSF1A gen	c 237	8	40.0	10	1	ABX79817	EST polymorphic DN
c 165	8.4	42.0	10	1	ADH62225	Human transcriptio	238	8	40.0	10	1	ACA94606	DNA tag from human
c 166	8.4	42.0	10	1	ADH75077	Photodamage detect	c 239	8	40.0	10	1	ACC41703	Zinc finger protei
c 167	8.4	42.0	10	1	ADH75117	Photodamage detect	c 240	8	40.0	10	1	ADG98554	Human CETP gene al
c 168	8.4	42.0	10	1	ADH75057	Photodamage marker	c 241	8	40.0	10	1	ADH78855	Human apical iodid
c 169	8.4	42.0	10	1	ADM77072	Photodamage marker							
c 170	8.4	42.0	10	1	ADM77132	Photodamage marker							
c 171	8.4	42.0	10	1	ADM77132	Photodamage marker							
c 172	8.4	42.0	10	1	ADH14419	Human retinoblasto							
c 173	8.4	42.0	10	1	ADH33248	Oligo SEQ ID 85, u							
c 174	8.4	42.0	10	1	ADO39842	Androgen-regulated							
c 175	8	40.0	9	1	AAQ96028	Oligonucleotide #1							
c 176	8	40.0	9	1	ADF67928	Human APC gene,-re							
c 177	8	40.0	9	1	ADR01088	Consensus interfe							
c 178	8	40.0	10	1	AAQ81105	Peptide nucleic ac							
c 179	8	40.0	10	1	AAQ81104	Peptide nucleic ac							

ALIGNMENTS

RESULT 1
AAC61866/c
ID AAC61866 standard; DNA; 20 BP.
XX
AAC61866;
XX

DT 06-MAR-2001 (first entry)

DE Antisense oligonucleotide directed against murine Fas (Apo-1) gene.

XX Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis;

XX Fas associated protein 1; protein tyrosine phosphatase; cancer;

XX autoimmune disease; inflammatory disease; lymphoma; phosphorothioate; ss.

XX Synthetic.

OS Mus musculus.

XX Key Location/Qualifiers

XX misc_feature 1..20

FT /tag= b

FT /note= "contains phosphorothioate linkages"

FT modified_base 1..5

FT /tag= a

FT /note= "2'-methoxyethoxy residues"

FT modified_base 16..20

FT /tag= c

FT /note= "2'-methoxyethoxy residues"

XX WO200061150-A1.

XX 19-OCT-2000.

XX 10-APR-2000; 2000WO-US009540.

XX 12-APR-1999; 99US-00290640.

XX (ISIS-) ISIS PHARM INC.

XX Dean NM, Marcusson EG;

XX WPI; 2000-628395/60.

XX Antisense oligonucleotides for treating hepatitis and colon, liver or

XX lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein 1

XX (Fap-1) expression.

XX Example 5; Page 55; 116pp; English.

XX AAC61860-78 represent antisense oligonucleotides which are directed

XX against nucleic acids encoding murine Fas (Apo-1). The specification

XX describes antisense compounds which are targeted to the 5'-untranslated

XX region, translational start site, translational termination region or 3'-

XX untranslated region of nucleic acid molecules encoding Fas, Fas ligand

XX (FasL), or Fap-1 (Fas associated protein 1, protein tyrosine

XX phosphatase). The antisense compounds are used to inhibit the expression

XX of Fas, FasL or Fap-1 in cells or tissues. They are used to treat

XX autoimmune or inflammatory diseases such as hepatitis. They can also be

XX used to treat cancer, especially colon, liver or lung cancer or lymphoma

XX

SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 616 CCGGAAAGAAAGTCTGGA 635

Db 20 CCGGAAAGAAAGTCTGGA 1

RESULT 2

ABN79656/c

ID ABN79656 standard; DNA; 20 BP.

XX AC ABN79656;

XX 29-JUL-2002 (first entry)

XX Mouse Fas chimeric phosphorothioate oligonucleotide #7.

XX Mouse; immunosuppressive; antiinflammatory; hepatotropic; cytostatic;

XX vasotropic; hepatitis; cancer; allograft rejection; ds; Fas.

XX Mus sp.

XX US2002004490-A1. _____

XX 10-JAN-2002.

XX 09-MAR-2001; 2001US-00802669.

XX 12-APR-1999; 99US-00290640.

XX 18-SEP-2000; 2000US-00665615.

XX (DEAN/) DEAN N M.

XX (MARC/) MARCUSSON E G.

XX (WYAT/) WYATT J.

XX (ZHAN/) ZHANG H.

XX Dean NM, Marcusson EG, Wyatt J, Zhang H;

XX WPI; 2002-204886/26.

XX Novel antisense compound targeted to nucleic acid encoding Fas, Fas

XX ligand or Fas associated protein-1 is useful for inhibiting expression of

XX Fas, Fas ligand, or Fap-1 in cells or tissues, and for treating

XX hepatitis.

XX Claim 23; Page 17; 84pp; English.

XX This invention relates to an antisense compound encoding Fas, Fas ligand,

XX or Fas associated protein-1 (Fap-1). The inhibition of Fas mediated

XX signalling is thought to be immunosuppressive, antiinflammatory,

XX hepatotropic, cytostatic and vasotropic. Antisense oligonucleotides were

XX designed to target human Fas. Oligonucleotides were synthesised as

XX chimeric oligonucleotides and are useful for treating an animal having an

XX autoimmune or inflammatory disease e.g., hepatitis, cancer, a condition

XX associated with apoptosis, allograft rejection, or ischemia reperfusion

XX injury. Optionally, the above mentioned conditions are prevented by

XX contacting the allograft with the antisense oligonucleotide. The

XX oligonucleotides are used in diagnostics, therapeutics, prophylaxis and

XX as research reagents and in kits. The oligonucleotides are also useful

XX for research purposes. The present nucleotide sequence is related to

XX mouse Fas

XX

SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 616 CCGGAAAGAAAGTCTGGA 635

Db 20 CCGGAAAGAAAGTCTGGA 1

RESULT 3

ABA00066/c

ID ABA00066 standard; DNA; 20 BP.

XX AC ABA00066;

XX 25-OCT-2002 (first entry)

XX Antisense oligonucleotide ISIS 220238.

XX Antisense; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..5

FT /*tag= a
FT /note= "2'-O-methoxyethyl ribose"
FT 16..20 b
FT /*tag= b
FT /note= "2'-O-methoxyethyl ribose"

PN WO200259137-A1.

XX 01-AUG-2002.

XX 23-OCT-2001; 2001WO-US049702.

XX 03-NOV-2000; 2000US-00705587.

XX (ISIS-) ISIS PHARM INC.

XX Yu Z, Baker BF, Wu J;

XX WPI; 2002-599758/64.

XX Detecting or quantitating oligonucleotides in a bodily fluid or extract
XX useful for studying pharmacokinetic properties of oligonucleotides in
XX humans comprising contacting the fluid or extract with a single-strand
XX specific nuclease.

XX Example 3; Page 5; 48pp; English.

XX The sequences given in ABA00064-67 are antisense oligonucleotides which
XX were detected using the method of the invention for detecting or
XX quantitating an oligonucleotide in a bodily fluid or extract. The method
XX comprises contacting the fluid or extract with a probe complementary to
XX the oligonucleotide, and with a single-strand specific nuclease under
XX conditions in which the probe which is not hybridized to the
XX oligonucleotide is degraded. The method is useful for detecting,
XX localizing and quantifying administered oligonucleotides in bodily fluids
XX and extracts taken from patients undergoing antisense oligonucleotide
XX therapy. The method is also useful for studying the pharmacokinetic
XX properties of oligonucleotides in animal models and in humans. The method
XX is highly sensitive through providing an increased detection of small
XX molecules when compared to traditional slab-gel electrophoresis

XX Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.6;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 616 CCGGAAAGAAAGTCTGGA 635

DB 20 CCGGAAAGAAAGTCTGGA 1

RESULT 4

AD133383/c

ID AD133383 standard; DNA; 20 BP.

XX AD133383;

XX 22-APR-2004 (first entry)

XX Labelled ISIS 22023 antisense DNA oligonucleotide SeqID 3.

XX antisense; body fluid; phosphorothioate backbone; 2' MOE;
XX methoxyethyl modification; antisense oligonucleotide therapy;
XX pharmacokinetic; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= b

FT /mod_base= OTHER

FT /note= "OTHER= phosphorothioate backbone"

FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 2' -O-methoxyethyl ribose"

FT modified_base 16..20 c

FT /*tag= c

FT /mod_base= OTHER
FT /note= "OTHER= 2' -O-methoxyethyl ribose"

XX US2004005618-A1.

XX 08-JAN-2004.

XX 27-MAY-2003; 2003US-00445996.

XX 03-NOV-2000; 2000US-00705587.

XX (YUZZ/) YU Z.

XX (BAKE/) BAKER B F.

XX (WUHH/) WU H.

XX Yu Z, Baker BF, Wu H;

XX WPI; 2004-081716/08.

XX Detecting antisense oligonucleotide in body fluid comprises forming
XX hybrids comprising oligonucleotide and probe complementary to
XX oligonucleotide and comprising detectable marker, degrading unhybridized
XX probe by nuclease.

XX Disclosure; SEQ ID NO 3; 20pp; English.

XX This invention relates to a novel method for detecting and quantitating
XX antisense oligonucleotides in a body fluid or extract. Specifically, it
XX comprises contacting the sample with a detectable, complementary probe to
XX form hybrid molecules that can bind to a solid support in order to
XX separate and identify the oligos of interest. The present invention
XX describes this method as useful for detecting antisense oligonucleotides
XX (20-30 nucleobases in length) in a bodily fluid such as plasma using a
XX probe that comprises at least one phosphorothioate linkage and a 2' MOE
XX (methoxyethyl) modification of at least one sugar moiety. The method can
XX be used to detect, localise and quantify administered oligonucleotides in
XX bodily fluids and extracts taken from patients undergoing antisense
XX oligonucleotide therapy and for studying the pharmacokinetic properties
XX of such oligos in animal models and in humans. The method is highly
XX sensitive (in the picomolar range) and provides improvements in detection
XX level sensitivity over the prior art that describe detection of modified
XX oligonucleotides only in the nanogram range. This oligonucleotide
XX sequence is an ISIS antisense oligo of the invention.

XX Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 20; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.6;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 616 CCGGAAAGAAAGTCTGGA 635

DB 20 CCGGAAAGAAAGTCTGGA 1

RESULT 5

ADL27712/c

ID ADL27712 standard; DNA; 20 BP.

XX ADL27712;

XX 20-MAY-2004 (first entry)

XX Mouse Fas cDNA, antisense oligonucleotide #7.

XX Antisense therapy; mouse; Fas; Fas ligand; FasL; Apo-1L; CD95L;

XX Fas associated protein 1; Fas-1; signal transduction; autoimmune disease;

KW inflammatory disease; cancer; immunosuppressive; antiinflammatory;
 KW cytostatic; phosphorothioate; ss.
 XX Mus musculus.

OS
 FH Key Location/Qualifiers
 FT modified_base 1..20

FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "This oligonucleotide has a phosphorothioate
 FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
 FT and 3' ends, which are 5 nucleotides in length at each
 FT end. All cytidine residues are 5-methylcytidines"
 XX

PN US6653133-B1.

XX 25-NOV-2003.

XX 18-SEP-2000; 2000US-00665615.

XX 12-APR-1999; 99US-00290640.

XX (ISIS-) ISIS PHARM INC.

PA Dean NM, Marcusson EG, Wyatt J;
 PI WPI; 2004-050524/05.

XX New antisense oligonucleotides of 20-50 nucleobases, useful for treating
 XX autoimmune or inflammatory diseases, and cancer.

PT Example 5; SEQ ID NO 73; 76pp; English.
 XX The present invention relates to antisense compounds targeted to nucleic
 XX acids encoding human Fas (also known as Apo-1 or CD95), Fas ligand (FasL,
 XX also Apo-1L and CD95L), and Fas associated protein 1 (Fap-1). The
 XX antisense compound comprises an antisense oligonucleotide that
 XX specifically hybridises with one of the said nucleic acids and inhibits
 XX Fas, FasL or Fap-1 mediated signal transduction. The antisense
 XX oligonucleotide is a chimeric oligonucleotide. The antisense
 XX oligonucleotide comprises at least one modified internucleoside linkage,
 XX preferably a phosphorothioate linkage. It also comprises at least one
 XX modified sugar moiety, preferably a 2'-O-methoxyethyl (2'-MOE) sugar
 XX moiety. The antisense oligonucleotide further comprises at least one
 XX modified nucleobase, preferably a 5-methylcytosine. The antisense
 XX oligonucleotides are useful for the treatment of autoimmune or
 XX inflammatory diseases, and cancers associated with overexpression of or
 XX constitutive activation of Fas, FasL, or Fap-1. The present sequence
 XX represents an antisense oligonucleotide used in the examples of the
 XX present invention.

XX Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 616 CCGGAAAAGAAAGTCTGGA 635
 DB 20 CCGGAAAAGAAAGTCTGGA 1
 |||||

RESULT 6

ADM53484/C

ID ADM53484 standard; DNA; 20 BP.

XX ADM53484;

XX 03-JUN-2004 (first entry)

XX Mouse Fas antisense oligonucleotide seqid 73.

XX immunosuppressive; antiinflammatory; hepatotropic; virucide; cytostatic;

KW

KW antisense technology; Fas; Fas ligand; Fap-1; Fas associated disorder;
 KW Fap-1 associated disorder; ischaemia reperfusion injury; apoptosis;
 KW allograft; autoimmune disease; inflammatory disease; hepatitis; cancer;
 XX lymphoma; mouse; antisense oligonucleotide; ss.

OS Mus musculus.

FH Key Location/Qualifiers
 FT modified_base 1..20

FT /*tag= b
 FT /mod_base= OTHER

FT /note= "OTHER= Phosphorothioate backbone. All cytidines
 FT are 5-methylcytidines"
 XX

FT modified_base 1..5

FT /*tag= a
 FT /mod_base= OTHER

FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
 XX

FT modified_base 15..20

FT /*tag= c
 FT /mod_base= OTHER

FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
 XX

PN US2004033979-A1.

XX 19-FEB-2004.

XX 14-JUL-2003; 2003US-00619220.

XX 12-APR-1999; 99US-00290640.

XX 18-SEP-2000; 2000US-00665615.

XX 09-MAR-2001; 2001US-00802669.

XX (DEAN/) DEAN N M.

XX (MARC/) MARCUSSON E G.

XX (WYAT/) WYATT J.

XX (ZHAN/) ZHANG H.

XX Dean NM, Marcusson EG, Wyatt J, Zhang H;
 XX WPI; 2004-180091/17.

XX New antisense compound targeted to nucleic acid molecule encoding Fas or
 XX Fap-1, useful in diagnosing, treating or preventing autoimmune or
 XX inflammatory disease, cancer, apoptosis, allograft rejection or ischemia
 XX reperfusion injury.

XX Claim 65; SEQ ID NO 73; 83pp; English.

XX The invention describes an antisense compound 8-30 or 8-50 nucleobases in
 XX length targeted to the 5'-untranslated region, translational start site,
 XX translational termination region or 3'-untranslated region of a nucleic
 XX acid molecule encoding Fas, Fas ligand or Fap-1. Also described are: a
 XX pharmaceutical composition comprising the anti-sense compound and a
 XX pharmaceutical carrier or diluent; a method of inhibiting the expression
 XX of Fas or Fap-1 in cells or tissues: treating an animal having a disease
 XX or condition associated with Fas or Fap-1; and/or preventing allograft
 XX rejection, ischaemia reperfusion injury or apoptosis in an allograft
 XX recipient. The antisense compound and pharmaceutical composition is
 XX useful in diagnosing, treating or preventing autoimmune or inflammatory
 XX disease, e.g. hepatitis, cancer, e.g. cancer of the colon, liver, lung or
 XX lymphoma, apoptosis, allograft rejection, e.g. cardiac, renal, hepatic
 XX or skin allograft and ischemia reperfusion injury. This sequence
 XX represents a mouse Fas antisense oligonucleotide.

XX Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 616 CCGGAAAAGAAAGTCTGGA 635

DB 20 CCGGAAAAGAAAGTCTGGA 1

|||||

RESULT 7
ADQ14990/c
ID ADQ14990 standard; DNA; 20 BP.
XX
AC ADQ14990;
XX
DT 07-OCT-2004 (first entry)
XX
DE Fatty acid synthase targeting oligonucleotide seqid 114.
XX
KW multifunctional oligomeric compound; RNA expression modulator;
KW double-stranded oligomeric compound; ss; antisense technology;
KW fatty acid synthase; antisense oligonucleotide.
XX
OS Homo sapiens.
XX
FN US2004137471-A1.
XX
PD 15-JUL-2004.
XX
PF 18-SEP-2003; 2003US-0066439.
XX
PR 18-SEP-2002; 2002US-0411780P.
XX
PA (VICK/) VICKERS T.
PA (KOO/) KOO S.
PA (BEN/) BENNETT C F.
PA (CROO/) CROOKE S T.
PA (DEAN/) DEAN N M.
PA (BAKE/) BAKER B F.
XX
PI Vickers T, Koo S, Bennett CF, Crooke ST, Dean NM, Baker BF;
XX
XX WPI; 2004-533354/51.
XX
XX Identifying a multifunctional oligomeric compound to modulate expression
PT of RNA comprises identifying an inhibiting antisense strand and
PT inhibiting double-stranded oligomeric compound as multifunctional
PT oligomeric compounds.
XX
XX Example 13; SEQ ID NO 114; 55pp; English.
XX
XX The invention describes a method of identifying a multifunctional
CC oligomeric compound to modulate expression of RNA. The method comprises:
CC contacting a target RNA with one or more double-stranded oligomeric
CC compounds hybridisable to one or more target regions of the RNA and
CC identifying double-stranded oligomeric compounds which inhibit target RNA
CC levels by at least 50%; contacting the target RNA with an antisense
CC strand of the modulating double-stranded oligomeric compound and
CC determining whether the antisense strand inhibits target RNA levels by at
CC least 50%; and identifying the inhibiting antisense strand and the
CC inhibiting double-stranded oligomeric compound as multifunctional
CC oligomeric compounds. Also described are: a multifunctional oligomeric
CC compound identified as above; a method for optimising target region
CC selection for modulation of RNA expression; a method of modulating RNA
CC expression; methods of optimising modulation of RNA; a method of
CC selecting a target region of a gene; a method of selecting an optimised
CC single-stranded oligomeric compound; a method of selecting an optimised
CC double-stranded oligomeric compound; a method of selecting a single-
CC stranded oligomeric compound; a method of selecting a double-stranded
CC oligomeric compound; a method of identifying one or more optimised double
CC -stranded oligomeric compounds; an oligomeric compound, 8-80 nucleobases
CC in length, targeted to a target RNA, where the oligomeric compound
CC specifically hybridises the target RNA and the oligomeric compound
CC inhibits RNA levels by at least 50% in both single-stranded and double-
CC stranded forms; and an oligomeric compound, 8-80 nucleobases in length
CC targeted to a target RNA, where the oligomeric compound has a least 80%
CC sequence homology to the complement of the target RNA and where the
CC oligomeric compound inhibits RNA levels by at least 60% in both single-
CC stranded and double-stranded forms. The method is useful for identifying
CC a multifunctional oligomeric compound to modulate expression of RNA. This

CC sequence represents a fatty acid synthase targeting oligonucleotide used
XX to control RNA expression levels.
SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 616 CCGGAAAGAAAGTGTGGA 635
DB 20 CCGGAAAGAAAGTGTGGA 1
RESULT 8
ADR06246/c
ID ADR06246 standard; DNA; 20 BP.
XX
AC ADR06246;
XX
DT 21-OCT-2004 (first entry)
XX
DE Fas antisense oligonucleotide seqid 247.
XX
KW cytostatic; gene therapy; apoptosis inhibitor;
KW radiation-induced apoptosis; tumour necrosis factor receptor 1; TNFR1;
KW mouse; antisense oligonucleotide; antisense technology; ss; Fas.
XX
OS Unidentified.
XX
PN US2004147471-A1.
XX
PD 29-JUL-2004.
XX
PF 06-NOV-2003; 2003US-00702817.
XX
PR 26-JUN-1998; 98US-00106038.
PR 17-JUN-1999; 99WO-US013763.
PR 24-OCT-2000; 2000US-00695451.
XX
XX (ZHAN/) ZHANG H.
XX
PI Zhang H;
XX
XX WPI; 2004-561407/54.
XX
XX Inhibiting radiation-induced apoptosis in a cell or tissue comprises
PT administering to the cell or tissue an antisense oligonucleotide targeted
PT to a nucleic acid molecule encoding tumor necrosis factor receptor 1.
XX
XX Example 23; SEQ ID NO 247; 24pp; English.
XX
XX The invention describes a method of inhibiting radiation-induced
CC apoptosis in a cell or tissue comprising administering to the cell or
CC tissue an antisense oligonucleotide of 8-30 nucleotides in length
CC targeted to a nucleic acid molecule encoding tumour necrosis factor
CC receptor 1 (TNFR1). The method and antisense oligonucleotides are useful
CC for inhibiting radiation-induced apoptosis in a cell or tissue, and for
CC treating diseases associated with the expression of TNFR1. This sequence
CC represents a Fas antisense oligonucleotide used in an assay to determine
CC the effect of antisense oligonucleotides on protection of the liver from
CC radiation-induced apoptosis.
XX
SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 616 CCGGAAAGAAAGTGTGGA 635
DB 20 CCGGAAAGAAAGTGTGGA 1

PR 23-SEP-1994; 94US-003111749.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Stinchcomb DT, Chowira B, Direnzo A, Draper KG, Dudycz LM;
 PI Grimm S, Karpelsky A, Kisch K, Matulic-Adamic J, McSwiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 DR Ribozyms having modified bases and methods for producing them - for use
 XX in inhibiting disease related genes.
 XX Claim 2; Page 214; 407pp; English.
 XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-
 CC 5) mRNA at the nucleotide base position indicated in the DE line. Regions
 CC of the mRNA that do not form secondary folding structures and that
 CC contain potential hammerhead and hairpin ribozyme cleavage sites were
 CC identified by computer analysis. Ribozymes directed against these mRNA
 CC sequences were designed and synthesised with modifications that improve
 CC their nuclease resistance. The ribozymes cleave the IL-5 target sequences
 CC and thereby inhibit IL-5 expression, making them useful for treating
 CC chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes
 CC and preventing the recruitment and activation of eosinophils. The
 CC ribozymes can also be used to treat eosinophilia (related to parasitic
 CC infection or with pulmonary infiltration) and L-tryptophan-associated
 CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
 CC field.)
 XX Sequence 15 BP; 2 A; 5 C; 2 G; 0 T; 6 U; 0 Other;
 SQ
 Query Match 62.0%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 30;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 618 GGAAGAAAGAAAGTGC 631
 DB 14 GCAAGAAAGAAAGTGC 1
 RESULT 11
 ID AAA06196 standard; DNA; 13 BP.
 XX AAA06196;
 AC AAA06196;
 XX 14-JUN-2000 (first entry)
 DT
 DE CFTR gene analysis oligonucleotide probe SEQ ID NO:206.
 DE
 KW CFTR; cystic fibrosis transmembrane conductance regulator; detection;
 KW mutation; probe; human; hybridisation; ss.
 XX Homo sapiens.
 OS
 XX US6027880-A.
 PN
 XX 22-FEB-2000.
 PD
 XX 10-OCT-1995; 95US-00544381.
 PF

XX 26-OCT-1993; 93US-00143312.
 PR 02-AUG-1994; 94US-00284064.
 PR 26-OCT-1994; 94WO-US012305.
 PR 02-AUG-1995; 95US-00510521.
 XX (AFFY-) AFFYMETRIX INC.
 XX Huang XC, Chee M, Lobban PE, Hubbell EA, Sheldon EL, Miyada CG;
 PI Cronin WT, Lipshutz RJ, Morris MS, Fodor SPA;
 XX WPI; 2000-194825/17.
 DR An array of nucleic acid probes immobilized on a solid support, useful
 XX for identifying mutations in the cystic fibrosis transmembrane
 PT conductance regulator.
 PT Disclosure; Col 143; 114pp; English.
 PS
 XX The present invention describes an array of nucleic acid probes
 CC immobilised on a solid support, which comprises: (1) a first probe set,
 CC comprising probes with a segment of at least 6 nucleotides complementary
 CC to the CFTR (cystic fibrosis transmembrane conductance regulator) gene,
 CC where the segment includes at least 1 interrogation position
 CC complementary to a nucleotide in the CFTR gene sequence; and (2) second,
 CC third and fourth probe sets, each comprising probes identical to those in
 CC (1) except that the interrogation position is occupied by a different
 CC nucleotide. AAA05991 to AAA06240 represent CFTR gene analysis
 CC oligonucleotide probes for use in the exemplification of the present
 CC invention. The present invention also describes a method of comparing a
 CC target nucleic acid with a reference sequence consisting of a
 CC predetermined sequence of nucleotides, comprising: (a) hybridising a
 CC sample comprising the target nucleic acid to an array of nucleic acid
 CC probes immobilised on a solid support; (b) comparing the relative
 CC specific binding of two corresponding probes from the first and second
 CC probe sets; (c) assigning a nucleotide in the target sequence as the
 CC complement of the interrogation position of the probe having the greater
 CC specific binding; and (d) repeating (b) and (c) by comparing the relative
 CC specific binding of a further two corresponding probes from the first and
 CC second probe sets until each nucleotide of interest in the target
 CC sequence has been assigned. The array is useful for analysis of the CFTR
 CC gene, e.g. detection of mutations
 XX
 XX Sequence 13 BP; 2 A; 2 C; 1 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 57.0%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 38;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 620 AAAAGAAAGTGC 632
 DB 13 AAAAGAAAGTGC 1
 RESULT 12
 ID ADF49014 standard; DNA; 13 BP.
 XX ADF49014;
 AC ADF49014;
 XX 12-FEB-2004 (first entry)
 DT
 DE DNA array associated probe #12.
 DE
 KW ss; DNA array; microfabricated array; DNA chip; CFTR gene mutation;
 KW cystic fibrosis gene; uncharacterised mutation identification;
 KW simultaneous screening; probe.
 XX Synthetic.
 OS
 XX US2003165823-A1.
 PN
 XX 04-SEP-2003.
 PD

XX 22-FEB-2000; 2000US-00510378.
 XX 26-OCT-1993; 93US-00143312.
 PR 02-AUG-1994; 94US-00284064.
 PR 26-OCT-1994; 94WO-US012305.
 PR 02-AUG-1995; 95US-00510521.
 PR 10-OCT-1995; 95US-00544381.
 XX (CRON/) CRONIN M T.
 PA (MIYA/) MIYADA C G.
 PA (HUBB/) HUBBELL E A.
 PA (CHEE/) CHEE M.
 PA (FODOR/) FODOR S P A.
 PA (HUANG/) HUANG X C.
 PA (LIPSHUTZ R J.)
 PA (LOBB/) LOBBAN P E.
 PA (MORRIS/) MORRIS M S.
 PA (SHELL/) SHELDON E L.
 XX Cronin MT, Miyada CG, Hubbell EA, Chee M, Fodor SPA, Huang XC;
 PI Lipshutz RJ, Lobban PE, Morris MS, Sheldon EL;
 XX WPI; 2004-020546/02.
 XX Arrays of oligonucleotide probes immobilized in microfabricated patterns
 PT on chips used for detecting mutations in the cystic fibrosis
 PT transmembrane conductance regulator (CFTR) gene.
 XX Disclosure; SEQ ID NO 206; 123pp; English.
 XX The invention relates to an array of oligonucleotide probes immobilised
 CC on a solid support, the array comprising at least two sets of
 CC oligonucleotide probes (a microfabricated array or DNA chip). The arrays
 CC can be used in methods to detect uncommon mutations in the CFTR gene.
 CC Prior art methods for analysis of the cystic fibrosis gene do not monitor
 CC large regions of the CFTR gene. The invention uses a large number of
 CC probes and therefore permits the identification of uncharacterised
 CC mutations and the simultaneous screening of large numbers of mutations
 CC with a high degree of accuracy. The present sequence is used in the
 CC exemplification of the invention.
 XX
 SQ Sequence 13 BP; 2 A; 2 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 57.0%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 38;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 620 AAAAGAAAGTGCT 632
 Db |||||
 13 AAAAGAAAGTACT 1
 RESULT 13
 AB178572
 ID AB178572 standard; DNA; 12 BP.
 AC AB178572;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide primer SEQ ID NO 378545 for detecting SNP TSC0062833.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PF 06-APR-2001; 2001WO-IB000713.
 PR 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 378545; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 8 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
 SQ Query Match 55.0%; Score 11; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 619 GAAAGAAAGT 629
 Db |||||
 1 GAAAGAAAGT 1
 RESULT 14
 ABH16792
 ID ABH16792 standard; DNA; 13 BP.
 AC ABH16792;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide SEQ ID NO 216769 for detecting SNP TSC0052691.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

CC	was obtained in electronic format from WIFO at					
XX	ftp.wipo.int/pub/published_pct_sequences					
CC						
SQ	Sequence 13 BP; 0 A; 5 C; 0 G; 8 T; 0 U; 0 Other;					
	Query Match	55.0%; Score 11; DB 1; Length 13;				
	Best Local Similarity	100.0%; Pred. No. 43;				
	Matches 11; Conservative	0; Mismatches	0; Indels	0; Gaps	0;	
Qy	618 GGAAAGGAAG 628					
Db	12 GGAAAGGAAG 2					
 RESULT 16						
ABF25014	ID ABF25014 standard; DNA; 13 BP.					
XX	AC AC					
XX	ABF25014;					
XX	21-FEB-2002 (first entry)					
DT	XX					
XX	XX					
DE	Oligonucleotide SEQ ID NO 125011 for detecting SNP TSC0031240.					
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;					
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;					
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.					
OS	Homo sapiens.					
XX	WO200177384-A2.					
PN	18-OCT-2001.					
PD	XX					
XX	06-APR-2001; 2001WO-IB000713.					
PF	XX					
XX	07-APR-2000; 2000DB-01019173.					
PR	XX					
XX	(EPIG-) EPIGENOMICS AG.					
PA	Olek A, Piepenbrock C, Berlin K;					
PI	WFI; 2001-657177/75.					
DR	Set of oligonucleotides, useful for diagnosis and cell typing, is					
XX	designed to detect single-nucleotide polymorphisms and cytosine					
PT	methylation status.					
PT	Claim 1; SEQ ID NO 125011; 29pp + Sequence Listing; German.					
XX	This invention describes novel oligonucleotide primers or peptide nucleic					
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)					
CC	and cytosine methylation status in chemically pretreated genomic DNA. The					
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a					
CC	range of diseases including immune system, gastrointestinal, respiratory,					
CC	central nervous system, cardiovascular and metabolic disorders. The					
CC	oligomers are also used for detecting cell type differentiation. ABC00010					
CC	-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073					
CC	represent the oligomers described in the invention. NOTE: The sequence					
CC	data for this patent did not form part of the printed specification, but					
CC	was obtained in electronic format from WIFO at					
CC	ftp.wipo.int/pub/published_pct_sequences					
XX	Sequence 13 BP; 9 A; 0 C; 3 G; 1 T; 0 U; 0 Other;					
SQ	Query Match	55.0%; Score 11; DB 1; Length 13;				
	Best Local Similarity	100.0%; Pred. No. 43;				
	Matches 11; Conservative	0; Mismatches	0; Indels	0; Gaps	0;	
Qy	620 AAAAGAAGTG 630					
Db	2 AAAAGAAGTG 12					

KW	central nervous system; gastrointestinal; respiratory; immune; metabolic;
XX	
OS	Homo sapiens.
XX	
PN	WO200177384-A2..
XX	
XX	18-OCT-2001.
PD	
XX	
PF	06-APR-2001; 2001WO-IB000713.
XX	
XX	
PR	07-APR-2000; 2000DE-01019173.
XX	
XX	(EPIG-) EPIGENOMICS AG.
PA	
XX	
PI	Olek A, Piepenbrock C, Berlin K;
XX	
XX	WPI; 2001-657177/75.
DR	
XX	
PT	Set of oligonucleotides, useful for diagnosis and cell typing, is
PT	designed to detect single-nucleotide polymorphisms and cytosine
PT	methylation status.
XX	
XX	
PS	Claim 1; SEQ ID NO 311275; 29pp + Sequence Listing; German.
XX	
CC	This invention describes novel oligonucleotide primers or peptide nucleic
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC	and cytosine methylation status in chemically pretreated genomic DNA. The
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC	range of diseases including immune system, gastrointestinal, respiratory,
CC	central nervous system, cardiovascular and metabolic disorders. The
CC	oligomers are also used for detecting cell type differentiation. ABC00010
CC	-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC	represent the oligomers described in the invention. NOTE: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
XX	
SQ	Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
	Query Match 52.0%; Score 10.4; DB 1; Length 12;
	Best Local Similarity 91.7%; Pred. No. 49;
	Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	619 GAAAGAAAGTG 630
Db	12 GTAAGAAAGTG 1
RESULT 19	
ABI40808/c	
ID	ABI40808 standard; DNA; 12 BP.
XX	
AC	ABI40808;
XX	
DT	22-FEB-2002 (first entry)
XX	
DE	Oligonucleotide primer SEQ ID NO 340781 for detecting SNP TSC0041677.
XX	
XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic;
XX	
OS	Homo sapiens.
XX	
PN	WO200177384-A2.
XX	
PD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-IB000713.
XX	
XX	
PR	07-APR-2000; 2000DE-01019173.
XX	
XX	(EPIG-) EPIGENOMICS AG.
PA	

XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 340781; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 2 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
 XX Query Match 52.0%; Score 10.4; DB 1; Length 12;
 XX Best Local Similarity 91.7%; Pred. No. 49;
 XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 618 GGAAGAGAAAGT 629
 DB 12 GGAAGATTAAGT 1
 ||||| |||||
 RESULT 20
 AB163850/c
 ID AB163850 standard; DNA; 12 BP.
 AC AB163850;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 363823 for detecting SNP TSC0054076.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 FN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 PR (EP1G-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 363823; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 1 A; 2 C; 1 G; 8 T; 0 U; 0 Other;
 XX Query Match 52.0%; Score 10.4; DB 1; Length 12;
 XX Best Local Similarity 91.7%; Pred. No. 49;
 XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 620 AAAAGAAAGTGC 631
 DB 12 AAAAGAAATGTC 1
 ||||| |||||
 RESULT 21
 ABH23500
 ID ABH23500 standard; DNA; 13 BP.
 AC ABH23500;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 223477 for detecting SNP TSC0054405.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 FN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 PR (EP1G-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 223477; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 8 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 53;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 618 GGAAAGAAAGT 629
 Db 1 GGAAAGAAAT 12

RESULT 22
 ABH23501/c
 ID ABH23501 standard; DNA; 13 BP.
 XX
 AC ABH23501;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 223478 for detecting SNP TSC0054405.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 223478; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 2 A; 3 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 53;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 618 GGAAAGAAAGT 629
 Db 13 GGAAAGAAAT 2

RESULT 23
 ABH62582
 ID ABH62582 standard; DNA; 13 BP.
 XX

AC ABH62582;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 262559 for detecting SNP TSC0063693.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 262559; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 8 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 53;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 618 GGAAAGAAAGT 629
 Db 2 GGAAAGAAAGT 13

RESULT 24
 ABH03129/c
 ID ABH03129 standard; DNA; 13 BP.
 XX
 AC ABH03129;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 203106 for detecting SNP TSC0049883.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.

XX FD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 203106; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX CC Sequence 13 BP; 2 A; 4 C; 0 G; 7 T; 0 U; 0 Other;

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX CC Sequence 13 BP; 2 A; 4 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. NO. 53;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAATGAAAGTG 630

DB 12 GAAATGAAAGTG 1

RESULT 25

ABC34591/c

ID ABC34591 standard; DNA; 13 BP.

XX AC ABC34591;

XX DT 20-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 34608 for detecting SNP TSC0011028.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.

XX PS Claim 1; SEQ ID NO 34608; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX CC Sequence 13 BP; 1 A; 6 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 1; Length 13;

Best Local Similarity 91.7%; Pred. NO. 53;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAAAGT 629

DB 12 GGAAGAAAGT 1

RESULT 26

ABF11491/c

ID ABF11491 standard; DNA; 13 BP.

XX AC ABF11491;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 111488 for detecting SNP TSC0027841.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 111488; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 3 C; 0 G; 8 T; 0 U; 1 Other;
 Query Match 52.0%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 53;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 618 GGAAAGAAAGT 629
 Db 13 GGAAAGAAAGT 2
 RESULT 27
 ABF91392
 ID ABF91392 standard; DNA; 13 BP.
 AC ABF91392;
 XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 191389 for detecting SNP TSC0047093.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 191389; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 52.0%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 53;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 622 AAGAAAGTGTG 633

Db 1 AAGAAAGTGTG 12
 RESULT 28
 ABF32303/C
 ID ABF32303 standard; DNA; 13 BP.
 XX
 AC ABF32303;
 XX
 DT 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 132300 for detecting SNP TSC0033007.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 132300; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 3 C; 0 G; 8 T; 0 U; 1 Other;
 Query Match 52.0%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 53;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 618 GGAAAGAAAGT 629
 Db 13 GGAAAGAAAGT 2
 RESULT 29
 ABF11490
 ID ABF11490 standard; DNA; 13 BP.
 XX
 AC ABF11490;
 XX
 DT 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 111487 for detecting SNP TSC0027841.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 11487; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 8 A; 0 C; 3 G; 1 T; 0 U; 1 Other;
 Query Match 52.0%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 53;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 618 GGAAAAGAAAGT 629
 Db 1 GGAAAAGAAAT 12
 RESULT 30
 ABC34590
 ID ABC34590 standard; DNA; 13 BP.
 AC ABC34590;
 XX
 XX 20-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 34607 for detecting SNP TSC0011028.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 34607; 29pp + Sequence Listing; German.

PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 34607; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 52.0%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 53;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 618 GGAAAAGAAAGT 629
 Db 2 GGAAAAGAAAT 13
 RESULT 31
 ABH03128
 ID ABH03128 standard; DNA; 13 BP.
 XX
 AC ABH03128;
 XX
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 203105 for detecting SNP TSC0049883.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 203105; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 7 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 53;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGAAAGTG 630
| | | | |
Db 2 GAAATGAAAGTG 13

RESULT 32
ABF32302
ID ABF32302 standard; DNA; 13 BP.
AC ABF32302;
XX
DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 132299 for detecting SNP TSC0033007.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX
PS Claim 1; SEQ ID NO 132299; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 8 A; 0 C; 3 G; 1 T; 0 U; 1 Other;

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 53;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 618 GGAAGAAAGAGT 629
| | | | |
Db 1 GAAAAGAAAGT 12

RESULT 33
ABH60877/C
ID ABH60877 standard; DNA; 13 BP.
XX
AC ABH60877;
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 260854 for detecting SNP TSC0063330.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX
PS Claim 1; SEQ ID NO 260854; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 2 A; 4 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 53;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGAAAGTG 630
| | | | |
Db 13 GAAAAGATAGTG 2

RESULT 34

ABH62583/c
ID ABH62583 standard; DNA; 13 BP.
XX
AC ABH62583;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 262560 for detecting SNP TSC0063693.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 262560 for detecting SNP TSC0063693.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 262560; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 53;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 618 GGAAGAAAGT 629
Db 12 GGAAGAAAGT 1
RESULT 35
ABH60876
ID ABH60876 standard; DNA; 13 BP.
XX
AC ABH60876;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 260853 for detecting SNP TSC0063330.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 260853; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Query Match 52.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 53;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 619 GAAAGAAAGT 630
Db 1 GAAAGATAGT 12
RESULT 36
ABF91393/c
ID ABF91393 standard; DNA; 13 BP.
XX
AC ABF91393;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 191390 for detecting SNP TSC0047093.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 191390; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 52.0%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 53;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 622 AAGAAAGTGCTG 633
 Db 13 AAGAAAGTGCTG 2
 |||||
 |||||
 RESULT 37
 AAX54622/C
 ID AAX54622 standard; DNA; 11 BP.
 XX
 AC AAX54622;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Endothelial moocyte activating factor antisense oligonucleotide.
 XX
 KW Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.
 XX
 OS Synthetic.
 XX
 XX WO9913886-A1.
 PN
 XX
 PD 25-MAR-1999.
 XX
 PF 17-SEP-1998; 98WO-US019419.
 XX
 PR 17-SEP-1997; 97US-0059160P.
 PR 09-JUN-1998; 98US-00093972.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 XX Nyce JW;
 PI
 XX WPI; 1999-229400/19.
 DR
 XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction.

XX Disclosure; Page 47; 120pp; English.
 XX
 CC The specification describes antisense oligonucleotides (AAX52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene initiation
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
 CC end and the juxta-section between coding and non-coding regions and all
 CC segments of RNAs encoding proteins associated with one or more diseases,
 CC conditions or mixtures. The antisense oligonucleotides may be derived
 CC from sequences AAX5272-74. These multiple target oligonucleotides
 CC (specifically AAX55180-271) can be used for the antisense treatment of
 CC diseases and conditions. Typical diseases and conditions are those
 CC associated with impaired respiration and inflammation, including lung
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
 CC acute asthma, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
 CC well as all types of cancers which may metastasize or have metastasized
 CC to the lungs, including breast and prostate cancer
 XX
 SQ Sequence 11 BP; 0 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
 Query Match 50.0%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 619 GAAAGAAAG 628
 Db 11 GAAAGAAAG 2
 |||||
 |||||
 RESULT 38
 AAX34069/C
 ID AAX34069 standard; DNA; 11 BP.
 XX
 AC AAX34069;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:1758.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200009525-A2.
 PN
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US017712.
 XX
 PR 03-AUG-1998; 98US-0095212P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 XX Nyce JW;
 PI
 XX WPI; 2000-205971/18.
 DR
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or

PT cancers.

PS Disclosure; Page 483; 1343pp; English.

XX The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antilasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing

XX

SQ Sequence 11 BP; 0 A; 4 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAGAAAG 628
 |||||
 Db 11 GAAAGAAAG 2

RESULT 39

AAF20191/c

ID AAF20191 standard; DNA; 11 BP.

XX

AC AAF20191;

XX

XX 14-MAR-2001 (first entry)

XX Human endothelial monocyte activating factor DNA fragment #1758.

XX Low adenine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antilasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

XX

OS Homo sapiens.

XX

XX WO200062736-A2.

XX

PD 26-OCT-2000.

XX

XX 24-MAR-2000; 2000WO-US008020.

PF

XX

PR 06-APR-1999; 99US-0127958P.

XX

XX (UYEC-) UNIV EAST CAROLINA.

PA

PA (NYCE/) NYCE J W.

XX

PI Nyce JW;

XX

DR WPI; 2000-679539/66.

XX

PT Low adenine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

PT

XX Claim 14; Page 207; 1592pp; English.

PS The present invention describes low adenine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antilasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with the lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

XX

SQ Sequence 11 BP; 0 A; 4 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAGAAAG 628
 |||||
 Db 11 GAAAGAAAG 2

RESULT 40

ABQ86415

ID ABQ86415 standard; cDNA; 11 BP.

XX

AC ABQ86415;

XX

XX 10-SEP-2002 (first entry)

XX

XX Human skin stress/ageing related EST SEQ ID NO 170.

DE

XX

XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

XX

XX Homo sapiens.

OS

XX

XX WO200253773-A2.

PN

XX

XX 11-JUL-2002.

XX

XX 20-DEC-2001; 2001WO-EP015178.

PF

XX

PR 03-JAN-2001; 2001DE-01000121.
 XX (HENK) HENKEL KGAA.
 PA Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-528865/56.
 XX Identifying genes involved in skin stress and aging, useful e.g. in
 PT screening for cosmetic or therapeutic agents, based on differential gene
 PT expression.
 XX Claim 8; Page 44; 325pp; German.
 PS
 XX The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention
 XX
 SQ Sequence 11 BP; 6 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 50.0%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 621 AAAGAAGCTG 630
 Db 1 AAAGAAGCTG 10
 RESULT 41
 ABS57226
 ID ABS57226 standard; DNA; 11 BP.
 XX
 AC ABS57226;
 XX
 DT 03-FEB-2003 (first entry)
 XX
 DE Retrotransposon insertion element 12.1 related nucleic acid.
 XX
 KW Retrotransposon insertion element 12.1; ss; tumour;
 KW embryonic development deformity; male sexual development anomaly;
 KW antagonist.
 XX
 OS Unidentified.
 XX
 PN CN1345734-A;
 XX
 PD 24-APR-2002.
 XX
 PF 22-SEP-2000; 2000CN-00125331.
 XX
 PR 22-SEP-2000; 2000CN-00125331.
 XX
 PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-567223/61.
 XX
 XX New retrotransposon insertion element 12.1 polypeptide containing inverse
 PT transcripase area and encoding polynucleotide, useful for treating
 PT embryonic development deformity, tumor and male sexual development
 PT anomaly.
 XX
 PS Disclosure; Page 1 (disclosure); 32pp; Chinese.

XX The present invention discloses a novel retrotransposon insertion element
 CC 12.1, polynucleotide coding for the polypeptide and method for producing
 CC this polypeptide by using DNA recombination technology. The invention
 CC also discloses the method for curing several diseases, such as embryonic
 CC development deformity, tumour and male sexual development anomaly by
 CC using the polypeptide. The invention also discloses an antagonist for
 CC resisting said polypeptide and its therapeutic action and also discloses
 CC the application of the polynucleotide for coding this novel
 CC retrotransposon insertion element 12.1. The sequence presented is the
 CC retrotransposon insertion element 12.1 related nucleic acid
 XX
 SQ Sequence 11 BP; 7 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 50.0%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 619 GAAAGAAAG 628
 Db 1 GAAAGAAAG 10
 RESULT 42
 ABV67006
 ID ABV67006 standard; cDNA; 11 BP.
 XX
 AC ABV67006;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 4792.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 157; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 6 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 621 AAAGAAAGTG 630
 |||||
 Db 1 AAAGAAAGTG 10
 |||||
 RESULT 43
 ABV63326
 ID ABV63326 standard; cDNA; 11 BP.
 XX
 AC ABV63326;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 1112.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 PS Disclosure; Page 55; 1345pp; German.
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 8 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 50.0%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 618 GGAAGAGAAA 627
 |||||
 Db 1 GGAAGAGAAA 10
 |||||
 RESULT 44
 ABV70747
 ID ABV70747 standard; cDNA; 11 BP.
 XX
 AC ABV70747;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 8533.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 PS Disclosure; Page 55; 1345pp; German.
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 8 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 50.0%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 618 GGAAGAGAAA 627
 |||||
 Db 1 GGAAGAGAAA 10
 |||||
 RESULT 45
 ABV68868/c
 ID ABV68868 standard; cDNA; 11 BP.
 XX
 AC ABV68868;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 6654.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX

XX
 AC ABV70747;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 8533.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 PS Claim 24; Page 273; 1345pp; German.
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 8 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 50.0%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 618 GGAAGAGAAA 627
 |||||
 Db 1 GGAAGAGAAA 10
 |||||
 RESULT 45
 ABV68868/c
 ID ABV68868 standard; cDNA; 11 BP.
 XX
 AC ABV68868;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 6654.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX

PN WO200253774-A2.
XX 11-JUL-2002.
XX 20-DEC-2001; 2001WO-EP015179.
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK) HENKEL KGAA.
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX Disclosure; Page 210; 1345pp; German.
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 1 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
Query Match 50.0%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 621 AAAGAAAGTG 630
Db 11 AAAGAAAGTG 2
RESULT 46
ABZ95885/c
ID ABZ95885 standard; DNA; 11 BP.
XX ABZ95885;
XX 17-OCT-2003 (first entry)
XX Human monocyte activating factor antisense fragment no.1745.
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX Homo sapiens.
XX WO200285308-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013135.
XX 24-APR-2001; 2001US-0286137P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX Disclosure; SEQ ID NO 11127; 872pp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytosstatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 11 BP; 0 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
Query Match 50.0%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 619 GAAAGAAAG 628
Db 11 GAAAGAAAG 2
RESULT 47
ABD19178/c
ID ABD19178 standard; DNA; 11 BP.
XX ABD19178;
XX 29-JUL-2004 (first entry)
XX Human monocyte activating factor DNA fragment 1745.
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiasthmatic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX Homo sapiens.
XX WO200285309-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013143.
XX 24-APR-2001; 2001US-0286036P.
XX

PA (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-093058/08.
 XX Pharmaceutical composition for treating asthma, has antisease
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX Claim 15; SEQ ID NO 11127; 763pp; English.
 XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, lung
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX Sequence 11 BP; 0 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
 SQ Query Match 50.0%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 619 GAAAGAGAAAG 628
 Db 11 GAAAGAGAAAG 2
 RESULT 48
 ADQ32097
 ID ADQ32097 standard; DNA; 11 BP.
 XX AC ADQ32097;
 XX 23-SEP-2004 (first entry)
 XX Human facial skin-associated DNA fragment SEQ ID NO 187.
 XX facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
 XX Homo sapiens.
 OS DE10260928-A1.
 XX PN

PD 08-JUL-2004.
 XX 20-DEC-2002; 2002DE-01060928.
 XX 20-DEC-2002; 2002DE-01060928.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Schlottmann K, Gassenmeier T, Holtkoetter O;
 PI Conrath M, Hofmann K;
 XX WPI; 2004-518855/50.
 XX In vitro identification of genes important for facial skin, useful for
 PT assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.
 XX Claim 9; SEQ ID NO 187; 577pp; German.
 XX This invention describes a novel in vitro method for identifying genes
 CC that are significant for facial skin in humans. The method comprises
 CC recovering, from facial skin, a first mixture of genetically expressed
 CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 CC their fragments), recovering a second, similar mixture from some other
 CC human tissue, preferably skin from a protected area, especially from the
 CC breast and subjecting the mixtures to serial analysis of gene expression
 CC (SAGE) to identify those genes for which expression is markedly different
 CC between facial skin and the other tissue. The invention also describes an
 CC in vitro method for determining homeostasis of human facial skin; a test
 CC kit which comprises a solid support (flexible or rigid) on which are
 CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic
 CC agents. ADQ1911-ADQ3511 represent human DNA Tag fragments used to
 CC identify the facial skin-associated genes described in the invention.
 XX Sequence 11 BP; 6 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
 SQ Query Match 50.0%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 621 AAAGAAAGTG 630
 Db 1 AAAGAAAGTG 10
 RESULT 49
 AAQ91300
 ID AAQ91300 standard; DNA; 12 BP.
 XX AC AAQ91300;
 XX 25-MAR-2003 (revised)
 DT 07-FEB-1996 (first entry)
 XX Circular oligonucleotide end joining oligonucleotide.
 XX Circular oligonucleotide; infection inhibitor; labelled probe;
 KW nuclease resistant; high selectivity; high affinity;
 KW gene expression inhibitor; end joining oligonucleotide; ss.
 XX Synthetic.
 OS US5426180-A.
 XX PN 20-JUN-1995.
 XX PD

PF 11-JAN-1993; 93US-00004800.
 PR 27-MAR-1991; 91US-00675843.
 PR 26-MAR-1992; 92US-00859922.
 PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
 XX Kool ET;
 PI WPI; 1995-230952/30.
 DR
 XX Prepn. of single-stranded circular oligo:nucleotide cpds. - using a
 PT linear pre-circle and an end-joining oligo:nucleotide to form distinct
 PT binding domains.
 XX
 PS Example 1; Fig 3; 43pp; English.
 XX
 CC AAQ91300 is a circular oligonucleotide end joining oligo, used in the
 CC prepn. of the circular oligos given in AAQ91296-98. Circular oligos can
 CC be used to inhibit viral infection and gene expression, or (when
 CC labelled) as probes for the detection of target sequences. Circular
 CC oligos are resistant to nucleases, and bind targets with higher
 CC selectivity and affinity than do linear oligos. (Updated on 25-MAR-2003
 CC to correct PF field.)
 XX
 SQ Sequence 12 BP; 9 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 50.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 619 GAAAGAAAG 628
 Db |||||
 3 GAAAGAAAG 12
 RESULT 50
 AA42866
 ID AA42866 standard; DNA; 12 BP.
 AC AA42866;
 XX
 DT 10-JUN-1997 (first entry)
 XX
 DE Single stranded circular oligonucleotide target sequence #2.
 KW single stranded; circular; target sequence; parallel; detection;
 KW binding domain; anti-parallel; loop domain; complementarity; ss;
 KW synthesis; regulation; drug delivery; biosynthesis; tumour cell.
 XX
 OS Synthetic.
 XX
 PN WO9630384-A1.
 XX
 PD 03-OCT-1996.
 XX
 PF 21-MAR-1996; 96WO-US003757.
 XX
 PR 30-MAR-1995; 95US-00413813.
 XX
 PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
 XX
 PI Kool ET;
 XX
 DR WPI; 1996-455262/45.
 XX
 PT Single stranded circular oligo:nucleotide comprising parallel and or anti
 PT -parallel binding domain - used to regulate biosynthesis of DNA, RNA or
 PT protein in targetted mammalian tumour cell in vivo.
 XX
 PS Example 2; Fig 2A; 195pp; English.
 XX
 CC The sequences given in AA42860-80 represent single stranded (ss)

CC circular oligonucleotides or their target sequences. The ss circular
 CC oligonucleotides comprise a parallel binding (P) domain, and/or an anti-
 CC parallel binding (AP) domain, and at least 1 loop domain. The P and AP
 CC domains have sufficient complementarity to bind detectably to 1 strand of
 CC a defined nucleic acid target. The P domain is capable of binding in a
 CC parallel manner to the target. The AP domain is capable of binding in an
 CC anti-parallel manner to the target and the ends of the P and AP domains
 CC are separated by the loop domains. The ss circular oligonucleotides can
 CC be used to regulate the synthesis of DNA, RNA or protein (pref. by DNA
 CC replication, DNA reverse transcription, RNA splicing, RNA
 CC polyadenylation, RNA translocation or protein translocation) by binding a
 CC target sequence in the template. They can also be used to deliver a drug
 CC to a specific cell type by administering a drug covalently bound to them
 CC (i.e. to regulate the biosynthesis of DNA, RNA or protein in a targetted
 CC mammalian tumour cell in vivo, without substantially altering the
 CC biosynthesis of the DNA). They can also be used to detect a target
 CC nucleic acid by detecting an oligonucleotide-target complex. The circular
 CC oligonucleotide can bind both single and double stranded target nucleic
 CC acids, and has enhanced stability, compared to linear forms. This
 CC sequence is specifically the target region for the ss circular
 CC oligonucleotide given in AA42863-64
 XX
 SQ Sequence 12 BP; 9 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 50.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 619 GAAAGAAAG 628
 Db |||||
 3 GAAAGAAAG 12
 RESULT 51
 AA42896
 ID AA42896 standard; RNA; 12 BP.
 AC AA42896;
 XX
 DT 10-JUN-1997 (first entry)
 XX
 DE Single stranded circular oligonucleotide RNA target region.
 KW single stranded; circular; target sequence; parallel; detection;
 KW binding domain; anti-parallel; loop domain; complementarity; ss;
 KW synthesis; regulation; drug delivery; biosynthesis; tumour cell.
 XX
 OS Synthetic.
 XX
 PN WO9630384-A1.
 XX
 PD 03-OCT-1996.
 XX
 PF 21-MAR-1996; 96WO-US003757.
 XX
 PR 30-MAR-1995; 95US-00413813.
 XX
 PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
 XX
 PI Kool ET;
 XX
 DR WPI; 1996-455262/45.
 XX
 PT Single stranded circular oligo:nucleotide comprising parallel and or anti
 PT -parallel binding domain - used to regulate biosynthesis of DNA, RNA or
 PT protein in targetted mammalian tumour cell in vivo.
 XX
 PS Example 9; Page 129; 195pp; English.
 XX
 CC The sequences given in AA42894-96 represent target sequences bound by
 CC the single stranded (ss) circular oligonucleotides of the invention.
 CC These target regions have different backbones to determine if this is
 CC important in the binding of the ss circular oligo's. The ss circular

oligonucleotides comprise a parallel binding (P) domain, and/or an anti-parallel binding (AP) domain, and at least 1 loop domain. The P and AP domains have sufficient complementarity to bind detectably to 1 strand of a defined nucleic acid target. The P domain is capable of binding in a parallel manner to the target. The AP domain is capable of binding in an anti-parallel manner to the target and the ends of the P and AP domains are separated by the loop domains. The ss circular oligonucleotides can be used to regulate the synthesis of DNA, RNA or protein (pref. by DNA replication, DNA reverse transcription, RNA splicing, RNA polyadenylation, RNA translocation or protein translocation) by binding a target sequence in the template. They can also be used to deliver a drug to a specific cell type by administering a drug covalently bound to them (i.e. to regulate the biosynthesis of DNA, RNA or protein in a targetted mammalian tumour cell in vivo, without substantially altering the biosynthesis of the DNA). They can also be used to detect a target nucleic acid by detecting an oligonucleotide- target complex. The circular oligonucleotide can bind both single and double stranded target nucleic acids, and has enhanced stability, compared to linear forms

Sequence 12 BP; 9 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAGGAAG 628
 |||||
 Db 1 GAAAGGAAG 10

RESULT 52
 AAT42895
 ID AAT42895 standard; DNA; 12 BP.

XX AAT42895;

DT 10-JUN-1997 (first entry)

DE Single stranded circular oligonucleotide DNA target region.

XX single stranded; circular; target sequence; parallel; detection;
 KW binding domain; anti-parallel; loop domain; complementarity; ss;
 KW synthesis; regulation; drug delivery; biosynthesis; tumour cell.

XX Synthetic.

XX WO9630384-A1.

XX 03-OCT-1996.

XX 21-MAR-1996; 96WO-US003757.

XX 30-MAR-1995; 95US-00413813.

XX (RESE) RESEARCH CORP TECHNOLOGIES INC.

XX Kool ET;

XX WPI; 1996-455262/45.

XX Single stranded circular oligo:nucleotide comprising parallel and or anti-parallel binding domain - used to regulate biosynthesis of DNA, RNA or protein in targetted mammalian tumour cell in vivo.

PS Example 9; Page 129; 195pp; English.

XX The sequences given in AAT42894-96 represent target sequences bound by the single stranded (ss) circular oligonucleotides of the invention. These target regions have different backbones to determine if this is important in the binding of the ss circular oligo's. The ss circular oligonucleotides comprise a parallel binding (P) domain, and/or an anti-parallel binding (AP) domain, and at least 1 loop domain. The P and AP domains have sufficient complementarity to bind detectably to 1 strand of

CC a defined nucleic acid target. The P domain is capable of binding in a parallel manner to the target. The AP domain is capable of binding in an anti-parallel manner to the target and the ends of the P and AP domains are separated by the loop domains. The ss circular oligonucleotides can be used to regulate the synthesis of DNA, RNA or protein (pref. by DNA replication, DNA reverse transcription, RNA splicing, RNA polyadenylation, RNA translocation or protein translocation) by binding a target sequence in the template. They can also be used to deliver a drug to a specific cell type by administering a drug covalently bound to them (i.e. to regulate the biosynthesis of DNA, RNA or protein in a targetted mammalian tumour cell in vivo, without substantially altering the biosynthesis of the DNA). They can also be used to detect a target nucleic acid by detecting an oligonucleotide- target complex. The circular oligonucleotide can bind both single and double stranded target nucleic acids, and has enhanced stability, compared to linear forms

Sequence 12 BP; 9 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAGGAAG 628
 |||||
 Db 1 GAAAGGAAG 10

RESULT 53
 AAT42867/C
 ID AAT42867 standard; DNA; 12 BP.

XX AAT42867;

XX 10-JUN-1997 (first entry)

DE Single stranded circular oligonucleotide target sequence #3.

XX single stranded; circular; target sequence; parallel; detection;
 KW binding domain; anti-parallel; loop domain; complementarity; ss;
 KW synthesis; regulation; drug delivery; biosynthesis; tumour cell.

XX Synthetic.

XX WO9630384-A1.

XX 03-OCT-1996.

XX 21-MAR-1996; 96WO-US003757.

XX 30-MAR-1995; 95US-00413813.

XX (RESE) RESEARCH CORP TECHNOLOGIES INC.

XX Kool ET;

XX WPI; 1996-455262/45.

XX Single stranded circular oligo:nucleotide comprising parallel and or anti-parallel binding domain - used to regulate biosynthesis of DNA, RNA or protein in targetted mammalian tumour cell in vivo.

XX Example 2; Fig 2B; 195pp; English.

XX The sequences given in AAT42860-80 represent single stranded (ss) circular oligonucleotides or their target sequences. The ss circular oligonucleotides comprise a parallel binding (P) domain, and/or an anti-parallel binding (AP) domain, and at least 1 loop domain. The P and AP domains have sufficient complementarity to bind detectably to 1 strand of a defined nucleic acid target. The P domain is capable of binding in a parallel manner to the target. The AP domain is capable of binding in an anti-parallel manner to the target and the ends of the P and AP domains are separated by the loop domains. The ss circular oligonucleotides can be used to regulate the synthesis of DNA, RNA or protein (pref. by DNA

CC replication, DNA reverse transcription, RNA splicing, RNA
CC polyadenylation, RNA translocation or protein translocation) by binding a
CC target sequence in the template. They can also be used to deliver a drug
CC to a specific cell type by administering a drug covalently bound to them
CC (i.e. to regulate the biosynthesis of DNA, RNA or protein in a targetted
CC mammalian tumour cell in vivo, without substantially altering the
CC biosynthesis of the DNA). They can also be used to detect a target
CC nucleic acid by detecting an oligonucleotide-target complex. The circular
CC oligonucleotide can bind both single and double stranded target nucleic
CC acids, and has enhanced stability, compared to linear forms
XX
SQ Sequence 12 BP; 0 A; 3 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAGAAAG 628
Db 10 GAAAGAAAG 1

RESULT 54
AAX54619/C
ID AAX54619 standard; DNA; 12 BP.

XX AAX54619;
AC
XX 05-JUL-1999 (first entry)
DT

XX Human P selectin antisense oligonucleotide fragments.

XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.

XX Synthetic.

XX WO9913886-A1.

XX 25-MAR-1999.

XX 17-SEP-1998; 98WO-US019419.

XX 17-SEP-1997; 97US-0059160P.

XX 09-JUN-1998; 98US-00093972.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 1999-229400/19.

XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction.

XX Disclosure; Page 47; 120pp; English.

XX The specification describes antisense oligonucleotides (AAX52869-X55271)
XX directed against at least 2 mRNAs selected from target genes, coding and
XX non-coding regions of RNAs corresponding to target genes, gene initiation
XX codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
XX end and the juxta-section between coding and non-coding regions and all
XX segments of RNAs encoding proteins associated with one or more diseases,
XX conditions or mixtures. The antisense oligonucleotides may be derived
XX from sequences AAX55272-74. These multiple target oligonucleotides

CC (specifically AAX55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX

SQ Sequence 12 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAGAAAG 628
Db 12 GAAAGAAAG 3

RESULT 55
AAX14828
ID AAX14828 standard; DNA; 12 BP.

XX AAX14828;

XX 24-MAR-1999 (first entry)
DT

XX Triple helix forming nucleotides 212-223 of 23S rRNA gene.

XX Triple-helix forming region; Triplex formation; DNA detection;
KW identification; bacteria; oncogene; virus; ds.

XX Escherichia coli.

XX US5861244-A.

XX 19-JAN-1999.

XX 22-DEC-1993; 93US-00173489.

XX 29-OCT-1992; 92US-00968436.

XX (PROF-) PROFILE DIAGNOSTIC SCI INC.

XX Hepburn AG, Wang C;

XX WPI; 1999-130384/11.

XX Assay of genetic sequences based on triplex formation from double
XX stranded analyte - and hybrid of an anchor and reporter sequences, with
XX reporter released if triplex formation occurs, used e.g. to identify
XX bacteria.

XX Disclosure; Col 21-22; 168pp; English.

XX The present sequence represents a potential triple-helix forming region.
XX It can be used to demonstrate the assay of the invention. The assay
XX comprises adding a sample containing double-stranded DNA test sequences,
XX e.g. containing the present sequence, to an aqueous medium containing at
XX least one complex of anchor DNA, attached to a solid support, and
XX reporter DNA, where either a part of the anchor DNA or reporter DNA is
XX designed to form a triple-strand structure with part of the test
XX sequence. Triplex formation results in displacement of the reporter DNA
XX which is detected as an indication of the presence of the DNA test
XX sequence. The method is used to detect DNA sequences, particularly for
XX identification of bacteria (by detecting genes for ribosomal RNA) in
XX clinical samples, but also detection of oncogenes and Hepatitis B virus

XX

SQ Sequence 12 BP; 8 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 GGAAGAAGAA 627
|||||

Db 3 GGAAGAAGAA 12

RESULT 56

AAA34066/c
ID AAA34066 standard; DNA; 12 BP.

XX

AC AAA34066;

XX

DT 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide SEQ ID NO:1755.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS
XX WO200009525-A2.

PN
XX 24-FEB-2000.

PD
XX 03-AUG-1999; 99WO-US017712.

PF
XX 03-AUG-1998; 98US-0095212P.

PR
XX (UYEC-) UNIV EAST CAROLINA.

PA
XX Nyce JW;

PI
XX WPI; 2000-205971/18.

DR
XX New antisense oligonucleotides useful for treating e.g. pulmonary

PT vasoconstriction, inflammation, allergies, asthma, hypertension, or

FT bronchitis, emphysema, respiratory distress syndrome, ischemia or

PT cancers.

XX Disclosure; Page 483; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ

CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing

XX SQ Sequence 12 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAAGAAAG 628
|||||

Db 12 GAAAAGAAAG 3

RESULT 57

AAF20188/c

ID AAF20188 standard; DNA; 12 BP.

XX

AC AAF20188;

XX

DT 14-MAR-2001 (first entry)

DE Human P selectin polynucleotide fragment #1755.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

XX Homo sapiens.

OS
XX WO2000062736-A2.

PN
XX 26-OCT-2000.

PD
XX 24-MAR-2000; 2000WO-US008020.

PF
XX 06-APR-1999; 99US-0127958P.

PR
XX (UYEC-) UNIV EAST CAROLINA.

PA
XX (NYCE/) NYCE J W.

PI
XX Nyce JW;

DR
XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger
CC adenosine receptors during metabolism, useful e.g. for treating cancers
CC and respiratory obstructions.

XX Claim 14; Page 206; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and

CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 12 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAGAAAG 628
 Db 12 GAAAGAAAG 3
 |||||

RESULT 58

ABI35504
 ID ABI35504 standard; DNA; 12 BP.

AC ABI35504;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 335477 for detecting SNP TSC0038849.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 335477; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 7 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 AAAAGAAAGT 629

Db 1 AAAAGAAAGT 10
 |||||

RESULT 59

ABI36919/C

ID ABI36919 standard; DNA; 12 BP.

AC ABI36919;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 336892 for detecting SNP TSC0039574.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 336892; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 1 A; 3 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 GAAAGAAAG 628
 |||||

XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 350690; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. The
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 9 A; 0 C; 2 G; 1 T; 0 U; 0 Other;
 SQ Query Match 50.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 620 AAAAGAAAGT 629
 Db 1 AAAAGAAAGT 10
 RESULT 63
 ABI49527/c
 ID ABI49527 standard; DNA; 12 BP.
 XX AC ABI49527;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 349500 for detecting SNP TSC0046174.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 349500; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. The
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 2 A; 2 C; 0 G; 8 T; 0 U; 0 Other;
 SQ Query Match 50.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 620 AAAAGAAAGT 629
 Db 12 AAAAGAAAGT 3
 RESULT 64
 ABI43842
 ID ABI43842 standard; DNA; 12 BP.
 XX AC ABI43842;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide primer SEQ ID NO 343815 for detecting SNP TSC0006945.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 343815; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. The
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 12 BP; 9 A; 0 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 620 AAAAGAAAGT 629
|||||
Db 3 AAAAGAAAGT 12
RESULT 65
ABI38926
ID ABI38926 standard; DNA; 12 BP.
AC
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 338899 for detecting SNP TSC0005508.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
AC ABI38926;
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 338899 for detecting SNP TSC0005508.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 338899; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 9 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 619 GAAAAGAAAG 628
|||||
Db 2 GAAAAGAAAG 11
RESULT 66
ABI79122/c

ABI79122 standard; DNA; 12 BP.
ABI79122;
22-FEB-2002 (first entry)
Oligonucleotide primer SEQ ID NO 379095 for detecting SNP TSC0004612.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB000713.
07-APR-2000; 2000DE-01019173.
(EPIC-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
Claim 1; SEQ ID NO 379095; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 12 BP; 3 A; 2 C; 0 G; 7 T; 0 U; 0 Other;
Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 620 AAAAGAAAGT 629
|||||
Db 12 AAAAGAAAGT 3
RESULT 67
ABZ95882/c
ID ABZ95882 standard; DNA; 12 BP.
XX
XX ABZ95882;
AC ABZ95882;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human P selectin fragment no.1742.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.
 XX Homo sapiens.
 OS WO200285308-A2.
 PN 31-OCT-2002.
 XX 23-APR-2002; 2002WO-US013135.
 XX 24-APR-2001; 2001US-0286137P.
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 DR
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 11124; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 0 Other;
 Query Match 50.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 619 GAAAGAAAG 628
 Db |||||||
 12 GAAAGAAAG 3
 RESULT 68
 ABD19173/C
 ID ABD19173 standard; DNA; 12 BP.
 XX
 AC ABD19173;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human P selectin DNA fragment 1742.
 XX
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;

KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ds.
 XX Homo sapiens.
 OS WO200285309-A2.
 PN 31-OCT-2002.
 XX 23-APR-2002; 2002WO-US013143.
 XX 24-APR-2001; 2001US-0286036P.
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-093058/08.
 DR
 XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 PS Claim 15; SEQ ID NO 11124; 763pp; English.
 XX
 CC This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 SQ Sequence 12 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 0 Other;
 Query Match 50.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 619 GAAAGAAAG 628
 Db |||||||
 12 GAAAGAAAG 3
 RESULT 69
 AAX14912
 ID AAX14912 standard; DNA; 11 BP.

XX AAX14912;
AC
XX 17-OCT-2003 (revised)
XX DT 24-MAR-1999 (first entry)
XX DE Triple helix forming nucleotides 595-605 of 23S rRNA gene.
XX KW Triple-helix forming region; Triplex formation; DNA detection;
XX KW identification; bacteria; oncogene; virus; ds.
XX OS Chlamydomophila caviae.
XX PN US5861244-A.
XX PD 19-JAN-1999.
XX PF 22-DEC-1993; 93US-00173489.
XX PR 29-OCT-1992; 92US-00968436.
XX PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX PI Hepburn AG, Wang C;
XX WPI; 1999-130384/11.
XX DR Assay of genetic sequences based on triplex formation from double
XX PT stranded analyte - and hybrid of anchor and reporter sequences, with
XX PT reporter released if triplex formation occurs, used e.g. to identify
XX PT bacteria.
XX PS Disclosure; Col 23-24; 168pp; English.
XX CC The present sequence represents a potential triple-helix forming region.
XX CC It can be used to demonstrate the assay of the invention. The assay
XX CC comprises adding a sample containing double-stranded DNA test sequences,
XX CC e.g. containing the present sequence, to an aqueous medium containing at
XX CC least one complex of anchor DNA, attached to a solid support, and
XX CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
XX CC designed to form a triple-strand structure with part of the test
XX CC sequence. Triplex formation results in displacement of the reporter DNA
XX CC which is detected as an indication of the presence of the DNA test
XX CC sequence. The method is used to detect DNA sequences, particularly for
XX CC identification of bacteria (by detecting genes for ribosomal RNA) in
XX CC clinical samples, but also detection of oncogenes and Hepatitis B virus.
XX CC (Updated on 17-OCT-2003 to standardise OS field)
XX SQ Sequence 11 BP; 6 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

XX Query Match 47.0%; Score 9.4; DB 1; Length 11;
XX Best Local Similarity 90.9%; Pred. No. 64;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX QY 618 GGAAGAAGAAAG 628
XX DB 1 GGAAGAAGAAAG 11

XX RESULT 70
XX ABQ87218
XX ID ABQ87218 standard; cDNA; 11 BP.
XX XX
XX AC ABQ87218;
XX DT 10-SEP-2002 (first entry)
XX DE Human skin stress/ageing related EST SEQ ID NO 973.
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX XX Homo sapiens.
XX OS

PN WO200253773-A2.
XX 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015178.
XX PR 03-JAN-2001; 2001DE-01000121.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-528865/56.
XX XX Identifying genes involved in skin stress and aging, useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential gene
XX PT expression.
XX XX Claim 8; Page 77; 325pp; German.
XX CC The invention relates to identifying (M1) genes in vitro that, in humans
XX CC or animals, are important for skin ageing and/or skin stress by serial
XX CC analysis of gene expression between mixtures of transcribed and
XX CC optionally translated, genetically encoded factors (A) obtained from
XX CC young and aged skin, to identify that genes that show strong differential
XX CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX CC useful for: identifying markers of skin ageing and/or stress; determining
XX CC skin ageing and/or stress; and identifying or determining the effects of
XX CC pharmaceutical or cosmetic agents for control of skin ageing. The present
XX CC sequence is one of a group of human skin ageing/stress related expressed
XX CC sequence tags (ABQ86246-ABQ87680) of the invention.
XX SQ Sequence 11 BP; 7 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

XX Query Match 47.0%; Score 9.4; DB 1; Length 11;
XX Best Local Similarity 90.9%; Pred. No. 64;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX QY 619 GAAAGAAAGT 629
XX DB 1 GAAAGAAAGT 11

XX RESULT 71
XX ABQ86792
XX ID ABQ86792 standard; cDNA; 11 BP.
XX XX
XX AC ABQ86792;
XX DT 10-SEP-2002 (first entry)
XX DE Human skin stress/ageing related EST SEQ ID NO 547.
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX XX Homo sapiens.
XX OS
XX PN WO200253773-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015178.
XX PR 03-JAN-2001; 2001DE-01000121.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-528865/56.
XX XX Identifying genes involved in skin stress and aging, useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential gene
XX PT

PT expression.
 PS Claim 8; Page 59; 325pp; German.
 CC The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention
 XX SQ Sequence 11 BP; 7 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 619 GAAAGAAAGT 629
 Db 1 GAAATAAAGT 11
 |||||
 RESULT 72
 ABV62223
 ID ABV62223 standard; cDNA; 11 BP.
 AC ABV62223;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 9.
 DE Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 PR (HENK) HENKEL KGAA.
 PA Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 DR WO200253774-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 26; 1345pp; German.
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 XX (EST) of the invention
 XX SQ Sequence 11 BP; 7 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 619 GAAAGAAAGT 629
 Db 1 GAAATAAAGT 11
 |||||
 RESULT 72
 ABV62223
 ID ABV62223 standard; cDNA; 11 BP.
 AC ABV62223;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 9.
 DE Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 PR (HENK) HENKEL KGAA.
 PA Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 DR WO200253774-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 26; 1345pp; German.
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 XX (EST) of the invention
 XX SQ Sequence 11 BP; 7 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 621 AAGAGAAAGTGC 631
 Db 11 AAGAGAAAGTGC 1
 |||||

CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 7 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 619 GAAAGAAAGT 629
 Db 1 GAAACAAAGT 11
 |||||
 RESULT 73
 ABV66475/c
 ID ABV66475 standard; cDNA; 11 BP.
 XX AC ABV66475;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 4261.
 DE Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 PN 11-JUL-2002.
 PD 20-DEC-2001; 2001WO-EP015179.
 PF 03-JAN-2001; 2001DE-01000127.
 PR (HENK) HENKEL KGAA.
 PA Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 DR In vitro identification of skin-expressed genes, useful for determining
 XX homeostasis and identifying cosmetic or pharmaceutical agents against
 XX e.g. skin cancer.
 XX Disclosure; Page 143; 1345pp; German.
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 1 A; 4 C; 1 G; 5 T; 0 U; 0 Other;
 Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 621 AAGAGAAAGTGC 631
 Db 11 AAGAGAAAGTGC 1
 |||||

RESULT 74
 ABV64622
 ID ABV64622 standard; cDNA; 11 BP.
 XX
 AC ABV64622;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 2408.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 92; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 7 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 7 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 619 GAAAGAAAGT 629
 DB 1 GAAATATAAGT 11
 XX
 RESULT 75
 ABV67434
 ID ABV67434 standard; cDNA; 11 BP.
 XX
 AC ABV67434;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 5220.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW

KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 169; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 5 A; 1 C; 2 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 622 AAGAAAGTGTCT 632
 DB 1 AAGAAAGTGTCT 11
 XX
 RESULT 76
 ABV69644
 ID ABV69644 standard; cDNA; 11 BP.
 XX
 AC ABV69644;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 7430.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Claim 24; Page 233; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX Sequence 11 BP; 7 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 619 GAAAGAAAGT 629
 DB ||||| |||||
 1 GAAACAAAGT 11
 RESULT 77
 ABX79771
 ID ABX79771 standard; cDNA; 11 BP.
 XX
 AC ABX79771;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE EST polymorphic DNA repeat polynucleotide #96.
 XX
 KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KW spinal atrophy; bulbar atrophy; epinocerebellar ataxia.
 XX
 OS Homo sapiens.
 XX
 PN US6472154-B1.
 XX
 PD 29-OCT-2002.
 XX
 PF 31-DEC-1999; 99US-00475947.
 XX
 PR 31-DEC-1999; 99US-00475947.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Garner HR, Wren JD, Minna JD, Fondon JW;
 XX
 DR WPI; 2003-208818/20.
 XX
 XX Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.

PS Example; Col 355; 588pp; English.
 XX
 CC The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs
 XX
 SQ Sequence 11 BP; 6 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 618 GGAAAGAAAG 628
 DB ||||| |||||
 1 GGAAAGGAAAG 11
 RESULT 78
 ADQ35627/C
 ID ADQ35627 standard; DNA; 11 BP.
 XX
 AC ADQ35627;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 444.
 XX
 KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
 XX
 OS Homo sapiens.
 XX
 PN DE10260931-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 20-DEC-2002; 2002DE-01060931.
 XX
 PR 20-DEC-2002; 2002DE-01060931.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 XX
 DR WPI; 2004-518857/50.
 XX
 PT In vitro identification of genes important for hair-bearing skin, useful
 PT for assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.
 XX
 PS Claim 5; SEQ ID NO 444; 250pp; German.
 XX
 CC This invention describes a novel in vitro method for identifying genes
 CC that are significant for hair-bearing skin in humans. The method
 CC comprises recovering, from hair-bearing skin, a first mixture of
 CC genetically expressed (transcribed and optionally translated) factors
 CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
 CC mixture from skin on which hair does not grow and subjecting both
 CC mixtures to serial analysis of gene expression (SAGE) to identify those
 CC genes for which expression is markedly different between the two types of

skin. The invention also describes in vitro methods for determining homeostasis of human hair-bearing skin and for determining activity of cosmetic and pharmaceutical agents for use against disorders or disturbances of the homeostasis of human hair-bearing skin. A biochip and a test kit comprising a solid support (flexible or rigid) with immobilised probes are also described for determining homeostasis. The hair-bearing skin is from the scalp and the other skin is from the face. The method allows identification of as many as possible of the genes important for hair-bearing skin, and therefore, of a very wide range of potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent human DNA Tag fragments used to identify genes associated with hair-bearing skin.

Sequence 11 BP; 3 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 622 AAGAAATGCT 632
DB 11 AAGAAATGCT 1

RESULT 79
ADQ35251
ID ADQ35251 standard; DNA; 11 BP.
XX AC ADQ35251;
XX DT 23-SEP-2004 (first entry)
XX DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 68.
XX KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
XX KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX OS Homo sapiens.
XX PN DE10260931-A1.
XX PD 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060931.
XX PR 20-DEC-2002; 2002DE-01060931.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Schlottmann K, Gassenmeier T, Holtkoetter O;
XX PI Conradt M, Hofmann K;
XX DR WPI; 2004-518857/50.
XX PS Claim 7; SEQ ID NO 68; 250pp; German.
XX PT In vitro identification of genes important for hair-bearing skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.
XX PT Claim 7; SEQ ID NO 68; 250pp; German.
XX CC This invention describes a novel in vitro method for identifying genes that are significant for hair-bearing skin in humans. The method comprises recovering, from hair-bearing skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from skin on which hair does not grow and subjecting both mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between the two types of skin. The invention also describes in vitro methods for determining homeostasis of human hair-bearing skin and for determining activity of cosmetic and pharmaceutical agents for use against disorders or disturbances of the homeostasis of human hair-bearing skin. A biochip and a test kit comprising a solid support (flexible or rigid) with

immobilised probes are also described for determining homeostasis. The hair-bearing skin is from the scalp and the other skin is from the face. The method allows identification of as many as possible of the genes important for hair-bearing skin, and therefore, of a very wide range of potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent human DNA Tag fragments used to identify genes associated with hair-bearing skin.

Sequence 11 BP; 7 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAAGAGAAAGT 629
DB 1 GAAAGAGAAAGT 11

RESULT 80
ADQ36508
ID ADQ36508 standard; DNA; 11 BP.
XX AC ADQ36508;
XX DT 23-SEP-2004 (first entry)
XX DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 1325.
XX KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
XX KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX OS Homo sapiens.
XX PN DE10260931-A1.
XX PD 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060931.
XX PR 20-DEC-2002; 2002DE-01060931.
XX PA (HENK) HENKEL KGAA.
XX PI Petersohn D, Schlottmann K, Gassenmeier T, Holtkoetter O;
XX PI Conradt M, Hofmann K;
XX DR WPI; 2004-518857/50.
XX PS Claim 4; SEQ ID NO 1325; 250pp; German.
XX PT In vitro identification of genes important for hair-bearing skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.
XX PT Claim 4; SEQ ID NO 1325; 250pp; German.
XX CC This invention describes a novel in vitro method for identifying genes that are significant for hair-bearing skin in humans. The method comprises recovering, from hair-bearing skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from skin on which hair does not grow and subjecting both mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between the two types of skin. The invention also describes in vitro methods for determining homeostasis of human hair-bearing skin and for determining activity of cosmetic and pharmaceutical agents for use against disorders or disturbances of the homeostasis of human hair-bearing skin. A biochip and a test kit comprising a solid support (flexible or rigid) with immobilised probes are also described for determining homeostasis. The hair-bearing skin is from the scalp and the other skin is from the face. The method allows identification of as many as possible of the genes important for hair-bearing skin, and therefore, of a very wide range of potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent

CC human DNA Tag fragments used to identify genes associated with hair-
bearing skin.
CC Sequence 11 BP; 7 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
SQ

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGAAAGT 629
|||||
Db 1 GAAACAAAGT 11

RESULT 81
ADQ36530
ID ADQ36530 standard; DNA; 11 BP.
XX
AC ADQ36530;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human Keratin 10 DNA fragment.
XX
KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX
OS Homo sapiens.
XX
PN DE10260931-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060931.
XX
PR 20-DEC-2002; 2002DE-01060931.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518857/50.
XX

In vitro identification of genes important for hair-bearing skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.

PS Disclosure; Page 13; 250pp; German.
XX

This invention describes a novel in vitro method for identifying genes that are significant for hair-bearing skin in humans. The method comprises recovering, from hair-bearing skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from some other human tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between facial skin and the other tissue. The invention also describes an in vitro method for determining homeostasis of human facial skin; a test kit which comprises a solid support (flexible or rigid) on which are immobilised probes that bind specifically to the factors of interest and a biochip for determining homeostasis of human facial skin. The products of the invention are also used in a method which determines activity of cosmetic and pharmaceutical agents for use against disorders or disturbances of the homeostasis of human skin and a screening method for identifying cosmetic and pharmaceutical agents. The method allows identification of as many as possible of the genes important for facial skin and thus of a very wide range of potential therapeutic and cosmetic agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to identify the facial skin-associated genes described in the invention.

SQ Sequence 11 BP; 7 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
XX

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGAAAGT 629
|||||
Db 1 GAAACAAAGT 11

RESULT 82
ADQ32783
ID ADQ32783 standard; DNA; 11 BP.
XX
AC ADQ32783;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human facial skin-associated DNA fragment SEQ ID NO 873.
XX
KW facial skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS Homo sapiens.
XX
PN DE10260928-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060928.
XX
PR 20-DEC-2002; 2002DE-01060928.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518855/50.
XX

In vitro identification of genes important for facial skin, useful for assessing homeostasis and in screening for pharmaceutical or cosmetic agents, based on differential expression analysis.

PS Claim 5; SEQ ID NO 873; 577pp; German.
XX

This invention describes a novel in vitro method for identifying genes that are significant for facial skin in humans. The method comprises recovering, from facial skin, a first mixture of genetically expressed (transcribed and optionally translated) factors (i.e. proteins, mRNA or their fragments), recovering a second, similar mixture from some other human tissue, preferably skin from a protected area, especially from the breast and subjecting the mixtures to serial analysis of gene expression (SAGE) to identify those genes for which expression is markedly different between facial skin and the other tissue. The invention also describes an in vitro method for determining homeostasis of human facial skin; a test kit which comprises a solid support (flexible or rigid) on which are immobilised probes that bind specifically to the factors of interest and a biochip for determining homeostasis of human facial skin. The products of the invention are also used in a method which determines activity of cosmetic and pharmaceutical agents for use against disorders or disturbances of the homeostasis of human skin and a screening method for identifying cosmetic and pharmaceutical agents. The method allows identification of as many as possible of the genes important for facial skin and thus of a very wide range of potential therapeutic and cosmetic agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to identify the facial skin-associated genes described in the invention.

SQ Sequence 11 BP; 5 A; 1 C; 2 G; 3 T; 0 U; 0 Other;
XX

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 622 AAGAAAGTGCT 632
 Db 1 AAGAAAGTGCT 11

RESULT 83
 ADQ34045
 ID ADQ34045 standard; DNA; 11 BP.
 XX
 AC ADQ34045;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human facial skin-associated DNA fragment SEQ ID NO 2135.
 XX
 KW facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
 XX
 OS Homo sapiens.
 XX
 PN DE10260928-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 20-DEC-2002; 2002DE-01060928.
 XX
 PR 20-DEC-2002; 2002DE-01060928.
 XX
 PA (HENK) HENKEL KGAA.
 XX

Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 Conradt M, Hofmann K;
 WPI; 2004-518855/50.

In vitro identification of genes important for facial skin, useful for
 assessing homeostasis and in screening for pharmaceutical or cosmetic
 agents, based on differential expression analysis.
 Claim 4; SEQ ID NO 2135; 577pp; German.

This invention describes a novel in vitro method for identifying genes
 that are significant for facial skin in humans. The method comprises
 recovering, from facial skin, a first mixture of genetically expressed
 (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 their fragments), recovering a second, similar mixture from some other
 human tissue, preferably skin from a protected area, especially from the
 breast and subjecting the mixtures to serial analysis of gene expression
 (SAGE) to identify those genes for which expression is markedly different
 between facial skin and the other tissue. The invention also describes an
 in vitro method for determining homeostasis of human facial skin; a test
 kit which comprises a solid support (flexible or rigid) on which are
 immobilised probes that bind specifically to the factors of interest and
 a biochip for determining homeostasis of human facial skin. The products
 of the invention are also used in a method which determines activity of
 cosmetic and pharmaceutical agents for use against disorders or
 disturbances of the homeostasis of human skin and a screening method for
 identifying cosmetic and pharmaceutical agents. The method allows
 identification of as many as possible of the genes important for facial
 skin and thus of a very wide range of potential therapeutic and cosmetic
 agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
 identify the facial skin-associated genes described in the invention.

Sequence 11 BP; 7 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 47.0%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 64;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 619 GAAAGAAAGT 629
 Db 1 GAAATAAGT 11

RESULT 84
 AAX14680
 ID AAX14680 standard; DNA; 10 BP.
 XX
 AC AAX14680;
 XX

DT 24-MAR-1999 (first entry)
 XX
 DE Triple helix forming nucleotides 34-43 of Esterase D gene.
 XX
 KW Triple-helix forming region; Triplex formation; DNA detection;
 KW identification; bacteria; oncogene; virus; ds.

OS Homo sapiens.
 XX
 PN US5861244-A.
 XX
 PD 19-JAN-1999.
 XX
 PF 22-DEC-1993; 93US-00173489.
 XX
 PR 29-OCT-1992; 92US-00968436.
 XX
 PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
 XX
 PI Hepburn AG, Wang C;
 XX
 DR WPI; 1999-130384/11.

Assay of genetic sequences based on triplex formation from double
 stranded analyte - and hybrid of anchor and reporter sequences, with
 reporter released if triplex formation occurs, used e.g. to identify
 bacteria.

Disclosure; Col 15-16; 168pp; English.

The present sequence represents a potential triple-helix forming region.
 It can be used to demonstrate the assay of the invention. The assay
 comprises adding a sample containing double-stranded DNA test sequences,
 e.g. containing the present sequence, to an aqueous medium containing at
 least one complex of anchor DNA, attached to a solid support, and
 reporter DNA, where either a part of the anchor DNA or reporter DNA is
 designed to form a triple-strand structure with part of the test
 sequence. Triplex formation results in displacement of the reporter DNA
 which is detected as an indication of the presence of the DNA test
 sequence. The method is used to detect DNA sequences, particularly for
 identification of bacteria (by detecting genes for ribosomal RNA) in
 clinical samples, but also detection of oncogenes and Hepatitis B virus

Sequence 10 BP; 7 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 618 GGAAGAGAA 626
 Db 2 GGAAGAGAA 10

RESULT 85
 AAZ81980/c
 ID AAZ81980 standard; DNA; 10 BP.

XX
 AC AAZ81980;
 XX
 DT 07-APR-2000 (first entry)

XX Metastatic breast tumour cell upregulated transcript tag #1214.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 XX WO9965928-A2.
 XX 23-DEC-1999.
 PD 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106079/09.
 DR Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 PS Claim 1; Page 91; 219pp; English.
 XX AA280767 to AA283941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942
 CC to AA286677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX Sequence 10 BP; 1 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 622 AAGAAAGTG 630
 DB 10 AAGAAAGTG 2
 RESULT 86
 AAA99861
 ID AAA99861 standard; DNA; 10 BP.
 XX AAA99861;
 AC
 XX 06-AUG-2003 (revised)
 DT 26-JAN-2001 (first entry)
 XX Prokaryote RT-PCR primer PCR3.
 DE

XX Prokaryote; gene identification; environmental stimulus; gene regulation;
 KW bioprocess fermentation; PCR primer; ss.
 XX Bacteria.
 XX WO200056936-A1.
 XX 28-SEP-2000.
 PD 24-MAR-2000; 2000WO-US007912.
 XX 25-MAR-1999; 99US-0126038P.
 PR (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX Bentley WE, Gill RT;
 PI WPI; 2000-587669/55.
 DR Performing differential display of prokaryotic mRNA by a RT (reverse
 PT transcriptase)/RAP (random arbitrary-primed) PCR based technique comprises
 PT using a unique combination of random primers in a single amplification
 PT step.
 XX Claim 1; Page 19; 63pp; English.
 PS The present invention is concerned with a method of differential display
 CC of prokaryotic mRNA by RT-PCR. This involves the amplification of the
 CC mRNA once, and the further amplification of the cDNA, rather than the
 CC repeated amplification of the mRNA sample. It also eliminates the need
 CC for sequencing gels, using Northern and total RNA dot blots to confirm
 CC differentially displayed transcript levels. The primers AAA9849-A99868
 CC were used in a reverse transcription PCR amplification, and primers
 CC AAA9869-A99876 were used to prepare probes for a Northern blot analysis.
 CC The method can be used to rapidly identify genes with increased or
 CC decreased transcription following environmental stimuli, in bioprocess
 CC fermentations, and to analyse gene regulation. (Updated on 06-AUG-2003 to
 CC correct OS field.)
 XX Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 626 AAGTCTCG 634
 DB 2 AAGTCTCG 10
 RESULT 87
 AAD15800
 ID AAD15800 standard; DNA; 10 BP.
 XX AAD15800;
 AC
 XX 15-NOV-2001 (first entry)
 DT Human interleukin 15 (IL-15) gene polymorphism detecting primer #4.
 XX
 DE Human; interleukin 15; IL-15; gene therapy; chromosome 4q31; infection;
 KW drug screening; anthropological lineage; paternity testing; HIV; primer;
 KW Human Immunodeficiency Virus; forensic application; T-cell leukaemia; ss.
 XX Homo sapiens.
 OS WO200158914-A2.
 XX 16-AUG-2001.
 PD 08-FEB-2001; 2001WO-US004130.
 XX

PN WO200107662-A1.
XX 01-FEB-2001.
PD 24-JUL-2000; 2000WO-US020114.
PF 22-JUL-1999; 99US-0145170P.
XX (GENA-) GENAISSANCE PHARM INC.
PA Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;
XX WPI; 2001-182805/18.
PI New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,
XX for gene therapy of inflammation and for establishing a genotype or
PT haplotype.
PT
PS Disclosure; Page 24; 118pp; English.
XX
CC This invention relates to a polynucleotide sequence that is a polymorphic
CC variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene
CC also referred to as cyclooxygenase 2. The human PTGS2 gene sequence
CC AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and
CC AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2
CC protein is represented by AAF80898. The invention includes PCR and
CC sequencing primers, and probes represented in AAF80898 - AAF81151 which
CC are used to isolate and characterise the PTGS2 gene sequence, and to
CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide
CC sequences are used to express variant PTGS2 proteins, for structural
CC analysis or drug-binding studies and also in gene therapy (either
CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are
CC useful for diagnosis, prognosis and therapy and analysis of the new, and
CC known, polymorphisms and used to determine PTGS2 haplotype and genotype,
CC especially for determining association between a particular trait, e.g. a
CC clinical response to drugs that target PTGS2 but also disease
CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly
CC used for developing diagnostic tests and treatments for immune-related
CC disorders such as arthritis and inflammation. The polymorphisms may also
CC be used to study expression and biological function of PTGS2. Transgenic
CC animals that express PTGS2 are used to study expression of PTGS2
CC isogenes, for in vivo drug screening and testing, and for assessing
CC effects of therapeutic agents
XX
SQ Sequence 10 BP; 0 A; 2 C; 0 G; 8 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 619 GAAAGAGAA 627
Db 10 GAAAGAGAA 2
|||||||
RESULT 90
AAAF34400/c
ID AAF34400 standard; DNA; 10 BP.
XX AAF34400;
AC
XX 23-MAR-2001 (first entry)
DT
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1139.
DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.

XX 21-DEC-2000.
PD 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UNJO) UNIV JOHNS HOPKINS.
PA Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
PI Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
PT
PS Example; Page 40; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 0 G; 7 T; 0 U; 0 Other;
Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 620 AAAAGAGAG 628
Db 9 AAAAGAGAG 1
|||||||
RESULT 91
AAAF36229
ID AAF36229 standard; DNA; 10 BP.
XX AAF36229;
AC
XX 23-MAR-2001 (first entry)
DT
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2968.
DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS
XX

OS Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 106; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;
SQ Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 617 CGGAAAGA 625
| | | | |
Db 2 CGGAAAGA 10
RESULT 92
AAF34017
ID AAF34017 standard; DNA; 10 BP.
XX AAF34017;
AC AAF34017;
XX 23-MAR-2001 (first entry)
DT 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:756.
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;
XX linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Claim 1; Page 402; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression
XX varies as in M1, where a test substance which modifies the expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF44084
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;
SQ Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 617 CGGAAAGA 625
| | | | |
Db 2 CGGAAAGA 10
RESULT 93
AAF35802
ID AAF35802 standard; DNA; 10 BP.
XX AAF35802;
AC AAF35802;
XX 23-MAR-2001 (first entry)
DT 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2541.
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2541.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 XX WO200077214-A2.
 PN
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 DR
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 90; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 7 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 618 GGAAAGAA 626
 |||||
 Db 2 GGAAAGAA 10
 RESULT 94
 AAF33691
 ID AAF33691 standard; DNA; 10 BP.
 XX
 AC AAF33691;
 XX

DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:430.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 DR
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Claim 1; Page 390; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 7 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 618 GGAAAGAA 626
 |||||
 Db 2 GGAAAGAA 10
 RESULT 95
 AAD25884/c
 ID AAD25884 standard; DNA; 10 BP.

XX AAD25884;
AC
XX 26-MAR-2002 (first entry)
DT
XX
DE Primer #6 to detect polymorphisms in human DTR gene.
XX
XX Human; polymorphic site; PS; diptheria toxin receptor; DTR; haplotype;
KW heparin-binding epidermal growth factor-like growth factor; therapy;
KW chromosome 5q23; transgenic animal; drug screening; tumour growth;
KW smooth muscle hyperplasia; atherosclerosis; primer; ss.
XX
XX Homo sapiens.
OS
XX WO200179233-A2.
PN
XX 25-OCT-2001.
PD
XX 16-APR-2001; 2001WO-US012302.
PF
XX 14-APR-2000; 2000US-0197375P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Choi JY, Kliem SE, Koshy B, Parks KE, Stephens JC;
PI
XX WPI; 2002-082745/11.
DR
XX
XX New nucleotide polymorphisms in the human diptheria toxin receptor,
PT heparin-binding epidermal growth factor-like growth factor (DTR) gene,
PT useful for screening or expressing proteins for treating diseases related
PT to DTR activity.
XX
XX Claim 18; Page 12; 66pp; English.
PS
XX
XX The present invention relates to an isolated polynucleotide, comprising
CC polymorphisms in the human diptheria toxin receptor, heparin-binding
CC epidermal growth factor-like growth factor (DTR) gene. DTR gene is
CC located on chromosome 5q23. The polynucleotide comprising polymorphisms
CC in the DTR gene is useful in studying the expression and function of DTR,
CC and in expressing DTR protein for use in screening candidate drugs to
CC treat diseases related to DTR activity. The methods and haplotypes are
CC useful in improving the efficiency and output of several steps in the
CC drug discovery and development process, including target validation,
CC identifying lead compounds, and early phase clinical trials. The kit and
CC method are useful for determining if an individual has one of the
CC haplotypes or haplotype pairs. The transgenic animals are useful for
CC studying expression of the DTR isogenes in vivo, for in vivo screening
CC and testing of drugs targeted against DTR protein, and for testing the
CC efficacy of therapeutic agents and compounds for tumour growth, smooth
CC muscle hyperplasia or atherosclerosis in a biological system. The present
CC sequence is a primer to detect polymorphisms in human DTR gene
XX
SQ Sequence 10 BP; 0 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 GGAAGAGAA 626
DB 9 GGAAGAGAA 1
|||||
RESULT 96
AAS95417
ID AAS95417 standard; DNA; 10 BP.
XX
AC AAS95417;
XX
XX 14-FEB-2002 (first entry)
DT
XX Human ICAM2 gene allele-specific oligonucleotide PCR primer #22.
DE

XX Human; intercellular adhesion molecule 2; ICAM2; haplotyping; ss;
KW haplotype pair; single nucleotide polymorphism; genotyping; PCR primer;
KW gene therapy; drug screening; anti-HIV; anti-inflammatory; probe;
KW human immunodeficiency virus; sequencing primer.
XX
XX Homo sapiens.
OS
XX WO200185918-A1.
PN
XX 15-NOV-2001.
PD
XX 07-MAY-2001; 2001WO-US014714.
PF
XX 05-MAY-2000; 2000US-0201946P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Chew A, Choi JY, Denton RR, Kliem SE, Lee HH, Nandabalan K;
PI
XX WPI; 2002-055590/07.
DR
XX Novel polynucleotide containing polymorphisms in intercellular adhesion
PT molecule 2 gene, useful in developing drugs for treating human
PT immunodeficiency virus infection and inflammatory diseases.
XX
XX Claim 18; Page 14; 81pp; English.
PS
XX
XX The invention relates to single nucleotide polymorphisms in the gene
CC encoding human intercellular adhesion molecule 2 (ICAM2). A method for
CC haplotyping the ICAM2 gene in an individual comprises identifying the
CC nucleotide at one or more polymorphic sites and determining whether one
CC of the copies of the gene is defined by one of the ICAM2 haplotypes given
CC in the specification or whether both copies are defined by a haplotype
CC pair. This method is useful in genotyping, whereby all possible haplotype
CC pairs can be assigned to specific genotypes. An association between a
CC trait and a haplotype or haplotype pair of the ICAM2 gene can be
CC identified by comparing the frequency of the haplotype or haplotype pair
CC in a population exhibiting the trait with the frequency of the haplotype
CC or haplotype pair in a reference population, where a higher haplotype
CC frequency in the trait population indicates the trait is associated with
CC the haplotype or haplotype pair. ICAM2 and its corresponding DNA are used
CC for studying the expression and function of ICAM2, for use in screening
CC for candidate drugs to treat diseases related to ICAM2 activity, such as
CC HIV infection and inflammatory diseases. The sequences are also useful
CC for studying the effect of variation on the biological activity of ICAM2
CC as well as on the binding affinity of candidate drugs targeting ICAM2.
CC Sequences AAS95362-AAS95417 and AAS95419-AAS95442 represent allele-
CC specific oligonucleotide probes, sequencing primers, PCR primers and cDNA
CC encoding human ICAM2
XX
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 626 AAGTGTCTGG 634
DB 2 AAGTGTCTGG 10
|||||
RESULT 97
AAD43659
ID AAD43659 standard; DNA; 10 BP.
XX
AC AAD43659;
XX
XX 14-NOV-2002 (first entry)
DT
XX Human interleukin 15 (IL15) gene polymorphism detecting primer #6.
DE
XX Human; interleukin 15; IL15; haplotype; polymorphic site; PS;
KW

KW drug screening; infection; human immunodeficiency virus; leukaemia;
 KW transgenic animal; anti-inflammatory; cytostatic; antibacterial;
 KW gene therapy; primer; ss.
 XX Homo sapiens.
 OS
 XX WO200263044-A2.
 PN
 XX 15-AUG-2002.
 PD
 XX 15-AUG-2001; 2001WO-US025470.
 PF
 XX 08-FEB-2001; 2001WO-US004130.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Anastasio AE, Chew A, Denton RR, Nandabalan K, Stephens JC;
 PI Tirrell C;
 PI
 XX WPI; 2002-636598/68.
 DR
 XX New genetic variants comprising haplotypes of the human interleukin 15
 XX (IL15) gene, useful for treating infections, human immunodeficiency virus
 XX or T cell leukemia, or for screening drugs for treating these diseases.
 XX
 PS Claim 18; Page 14; 84pp; English.
 XX
 CC The invention relates to an isolated polynucleotide, which comprises
 CC polymorphisms in the human interleukin 15 (IL15) gene. The polynucleotide
 CC comprises genes and haplotypes of the IL15 gene. The polynucleotide
 CC comprises polymorphic sites referred to as PSI-13 to designate the order
 CC in which they are located in the gene. The polynucleotide comprising
 CC polymorphisms in the IL15 gene is useful in screening candidate drugs to
 CC treat diseases associated to IL15 activity, e.g. infections, human
 CC immunodeficiency virus or T cell leukaemia. The IL15 isogenes are
 CC especially useful for treating these diseases. The methods and haplotypes
 CC are useful in improving the efficiency of drug discovery and development
 CC processes, or for designing clinical trials of candidate drugs for
 CC treating the specific condition or disease. The transgenic animals are
 CC useful for studying expression of the IL15 isogenes in vivo, for in vivo
 CC screening and testing of drugs targeted against IL15 protein, and for
 CC testing the efficacy of the therapeutic agents. The present sequence is
 CC human IL15 gene polymorphism detecting primer
 XX
 SQ Sequence 10 BP; 8 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 620 AAAAGAAAG 628
 DB 2 AAAAGAAAG 10
 |||||
 RESULT 98
 AAD43657
 ID AAD43657 standard; DNA; 10 BP.
 XX
 AC AAD43657;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Human interleukin 15 (IL15) gene polymorphism detecting primer #4.
 XX
 KW Human; interleukin 15; IL15; haplotype; polymorphic site; PS;
 KW drug screening; infection; human immunodeficiency virus; leukaemia;
 KW transgenic animal; anti-inflammatory; cytostatic; antibacterial;
 KW gene therapy; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200263044-A2.

XX 15-AUG-2002.
 PD
 XX 15-AUG-2001; 2001WO-US025470.
 PF
 XX 08-FEB-2001; 2001WO-US004130.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Anastasio AE, Chew A, Denton RR, Nandabalan K, Stephens JC;
 PI Tirrell C;
 PI
 XX WPI; 2002-636598/68.
 DR
 XX New genetic variants comprising haplotypes of the human interleukin 15
 XX (IL15) gene, useful for treating infections, human immunodeficiency virus
 XX or T cell leukemia, or for screening drugs for treating these diseases.
 XX
 PS Claim 18; Page 14; 84pp; English.
 XX
 CC The invention relates to an isolated polynucleotide, which comprises
 CC polymorphisms in the human interleukin 15 (IL15) gene. The polynucleotide
 CC comprises genes and haplotypes of the IL15 gene. The polynucleotide
 CC comprises polymorphic sites referred to as PSI-13 to designate the order
 CC in which they are located in the gene. The polynucleotide comprising
 CC polymorphisms in the IL15 gene is useful in screening candidate drugs to
 CC treat diseases associated to IL15 activity, e.g. infections, human
 CC immunodeficiency virus or T cell leukaemia. The IL15 isogenes are
 CC especially useful for treating these diseases. The methods and haplotypes
 CC are useful in improving the efficiency of drug discovery and development
 CC processes, or for designing clinical trials of candidate drugs for
 CC treating the specific condition or disease. The transgenic animals are
 CC useful for studying expression of the IL15 isogenes in vivo, for in vivo
 CC screening and testing of drugs targeted against IL15 protein, and for
 CC testing the efficacy of the therapeutic agents. The present sequence is
 CC human IL15 gene polymorphism detecting primer
 XX
 SQ Sequence 10 BP; 8 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 620 AAAAGAAAG 628
 DB 1 AAAAGAAAG 9
 |||||
 RESULT 99
 AAS95574
 ID AAS95574 standard; DNA; 10 BP.
 XX
 AC AAS95574;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human IL8RB gene allele-specific oligonucleotide PCR primer #17.
 XX
 KW Human; interleukin 8 receptor beta; IL8RB; ss; antiinflammatory; probe;
 KW haplotyping; haplotype pair; single nucleotide polymorphism; genotyping;
 KW gene therapy; drug screening; chronic obstructive pulmonary disease;
 KW inflammatory disease; sequencing primer; PCR primer.
 XX
 OS Homo sapiens.
 XX
 PN WO200179221-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-US011942.
 XX
 PR 12-APR-2000; 2000US-0196734P.
 XX

(GENA-) GENAISSANCE PHARM INC.

Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;

WPI; 2002-055250/07.

New polymorphic variants comprising interleukin-8 receptor beta (IL8RB) isogene, useful in expressing IL8RB protein for use in screening for candidate drugs to treat diseases related to IL8RB activity, e.g. inflammatory disorders.

Claim 18; Page 14; 74pp; English.

The invention relates to single nucleotide polymorphisms in the human interleukin 8 receptor beta (IL8RB) gene. A method for haplotyping the IL8RB gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the IL8RB haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype pairs can be assigned to specific genotypes. An association between a trait and a haplotype or haplotype pair of the IL8RB gene can be identified by comparing the frequency of the haplotype or haplotype pair in a population exhibiting the trait with the frequency of the haplotype or haplotype pair in a reference population, where a higher haplotype frequency in the trait population indicates the trait is associated with the haplotype or haplotype pair. IL8RB and its corresponding DNA are used for studying the expression and function of IL8RB, for use in screening for candidate drugs to treat diseases related to IL8RB activity, such as chronic obstructive pulmonary disease and other inflammatory disorders. The sequences are also useful for studying the effect of variation on the biological activity of IL8RB as well as on the binding affinity of candidate drugs targeting IL8RB. Sequences AAS95525-AAS95579 represent allele-specific oligonucleotide probes, sequencing primers and PCR primers used to detect IL8RB gene polymorphisms

Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 620 AAAAGAAAG-628

Db 2 AAAAGAAAG 10

RESULT 100

ABX79795
ID ABX79795 standard; cDNA; 10 BP.

XX AC ABX79795;

DT 17-APR-2003 (first entry)

XX EST polymorphic DNA repeat polynucleotide #120.

DE EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX Homo sapiens.

OS US6472154-B1.

XX 29-OCT-2002.

XX 31-DEC-1999; 99US-00475947.

XX 31-DEC-1999; 99US-00475947.

(TEXA) UNIV TEXAS SYSTEM.

Garner HR, Wren JD, Minna JD, Fondon JW;

WPI; 2003-208818/20.

Identifying a candidate polymorphic repeat within a coding sequence, for understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability.

Example; Col 497; 588pp; English.

The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic, marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia, myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTs

Sequence 10 BP; 8 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 620 AAAAGAAAG-628

Db 2 AAAAGAAAG 10

RESULT 101

ACC41721
ID ACC41721 standard; DNA; 10 BP.

XX AC ACC41721;

XX 21-MAY-2003 (first entry)

XX Zinc finger protein DNA-binding domain target sequence SEQ ID NO:268.

DE Zinc finger domain; zinc finger; zinc finger binding domain; probe;
KW chimeric nucleic acid; library; PCR primer; ss.

XX Synthetic.

XX WO2003016571-A1.

XX 27-FEB-2003.

XX 17-AUG-2002; 2002WO-KR001560.

XX 17-AUG-2001; 2001US-0313402P.

XX 22-APR-2002; 2002US-0374355P.

XX (TOOL-) TOOLGEN INC.

XX Kim J, Bae K, Park K, Kwon Y, Ryu E, Hwang M;

XX WPI; 2003-268344/26.

XX New library comprising polypeptides having zinc finger domains, useful for producing chimeric nucleic acids.

XX PS Claim 40; Page 105; 234pp; English.

XX CC The present invention describes a library comprising polypeptides. Each

CC polypeptide comprises a first or second zinc finger domain. The domains

CC of each polypeptide are identical to a zinc finger domain from a

CC naturally occurring protein and either do not occur in the same naturally

CC occurring protein or occur in the same naturally occurring protein in a

CC different configuration than in the polypeptide. The domains vary among

CC polypeptides. Also described: (1) producing chimeric nucleic acids; (2)

CC generating an artificial zinc finger polypeptide that specifically binds

CC to a target DNA site; and (3) identifying a nucleic acid encoding a zinc

CC finger polypeptide that specifically recognises a target DNA site. The

CC library can be used for producing chimeric nucleic acids. ACC41551 to

CC ACC41758 and ABR40919 to ABR41015 represent nucleotide and amino acid

CC sequences given in the exemplification of the present invention

XX SQ Sequence 10 BP; 8 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAGAA 627

Db 2 GAAAGAGAA 10

|||||

RESULT 102

AAX14686

ID AAX14686 standard; DNA; 11 BP.

AC AAX14686;

XX 24-MAR-1999 (first entry)

XX Triple helix forming nucleotides 777-787 of Esterase D gene.

DE Triple-helix forming region; Triplex formation; DNA detection;

KW identification; bacteria; oncogene; virus; ds.

XX Homo sapiens.

XX US5861244-A.

PN 19-JAN-1999.

PD 22-DEC-1993; 93US-00173489.

PF 29-OCT-1992; 92US-00968436.

PR (PROF-) PROFILE DIAGNOSTIC SCI INC.

PA Hepburn AG, Wang C;

PI WPI; 1999-130384/11.

DR Assay of genetic sequences based on triplex formation from double

PT stranded analyte - and hybrid of anchor and reporter sequences, with

PT reporter released if triplex formation occurs, used e.g. to identify

PT bacteria.

XX Disclosure; Col 15-16; 168pp; English.

XX The present sequence represents a potential triple-helix forming region.

CC It can be used to demonstrate the assay of the invention. The assay

CC comprises adding a sample containing double-stranded DNA test sequences,

CC e.g. containing the present sequence, to an aqueous medium containing at

CC least one complex of anchor DNA, attached to a solid support, and

CC reporter DNA, where either a part of the anchor DNA or reporter DNA is

CC designed to form a triple-strand structure with part of the test

CC sequence. Triplex formation results in displacement of the reporter DNA

CC which is detected as an indication of the presence of the DNA test

CC sequence. The method is used to detect DNA sequences, particularly for

CC identification of bacteria (by detecting genes for ribosomal RNA) in

CC clinical samples, but also detection of oncogenes and Hepatitis B virus

XX SQ Sequence 11 BP; 9 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 74;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAGAA 627

Db 2 GAAAGAGAA 10

|||||

RESULT 103

ABQ87041

ID ABQ87041 standard; cDNA; 11 BP.

XX ABQ87041;

AC 10-SEP-2002 (first entry)

DT Human skin stress/ageing related EST SEQ ID NO 796.

DE Human; skin ageing; skin stress; EST; expressed sequence tag; ss.

XX Homo sapiens.

OS WO200253773-A2.

PN 11-JUL-2002.

PD 20-DEC-2001; 2001WO-EP015178.

PF 03-JAN-2001; 2001DE-01000121.

PR (HENK) HENKEL KGAA.

XX Petersohn D, Conradt M, Hofmann K;

PI WPI; 2002-528865/56.

DR Identifying genes involved in skin stress and aging, useful e.g. in

PT screening for cosmetic or therapeutic agents, based on differential gene

PT expression.

XX Claim 8; Page 70; 325pp; German.

XX The invention relates to identifying (M1) genes in vitro that, in humans

CC or animals, are important for skin ageing and/or skin stress by serial

CC analysis of gene expression between mixtures of transcribed and

CC optionally translated, genetically encoded factors (A) obtained from

CC young and aged skin, to identify that genes that show strong differential

CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is

CC useful for: identifying markers of skin ageing and/or stress; determining

CC skin ageing and/or stress; and identifying or determining the effects of

CC pharmaceutical or cosmetic agents for control of skin ageing. The present

CC sequence is one of a group of human skin ageing/stress related expressed

CC sequence tags (ABQ86246-ABQ87680) of the invention

XX SQ Sequence 11 BP; 8 A; 0 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 74;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAGAA 627

Db 3 GAAAGAGAA 11

|||||

RESULT 104

XX WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 XX Claim 24; Page 250; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 5 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 622 AAGAAAGTG 630
 |||||
 Db 3 AAGAAAGTG 11
 RESULT 107
 ADO26297
 ID ADO26297 standard; DNA; 11 BP.
 XX
 AC ADO26297;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human chondromedin protein related oligonucleotide #9.
 XX
 KW human; osteopathic; antiarthritic; antirheumatic; chondromedin; marker;
 KW ds.
 OS Unidentified.
 XX
 PN WO2004039974-A1.
 XX
 PD 13-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-JP013919.
 XX
 PR 30-OCT-2002; 2002JP-00315573.
 PR 28-NOV-2002; 2002JP-00345601.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Watanabe T, Inazuka M;
 XX
 DR WPI; 2004-390322/36.
 XX
 PT Novel chondromedin protein or salts, useful as diagnostic markers for
 PT osteitis, arthritis and for screening compounds useful in treating bone
 PT and articular diseases such as fracture, osteoarthritis, rheumatoid
 PT arthritis.
 XX
 XX Example 3; Page 75; 107pp; Japanese.
 PS
 XX The present invention relates to mature and precursor chondromedin
 CC protein sequences. Also provided are the coding sequences. The sequences
 CC are useful for preventing and/or treating bone and articular diseases

CC such as fracture, chondrodystrophy, osteodystrophy, osteoporosis,
 CC osteoarthritis, rheumatoid arthritis, synovitis and metabolic arthritis,
 CC and as markers in the diagnosis of the above conditions. The present
 CC invention is a polynucleotide sequence shown in the exemplification of the
 XX invention.
 SQ Sequence 11 BP; 7 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 45.0%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 618 GGAAAAGAA 626
 |||||
 Db 3 GGAAAAGAA 11
 RESULT 108
 ADO33318
 ID ADO33318 standard; DNA; 11 BP.
 XX
 AC ADO33318;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human facial skin-associated DNA fragment SEQ ID NO 1408.
 XX
 KW facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
 XX
 OS Homo sapiens.
 XX
 PN DE10260928-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 20-DEC-2002; 2002DE-01060928.
 XX
 PR 20-DEC-2002; 2002DE-01060928.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Schlottmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 XX
 DR WPI; 2004-518855/50.
 XX
 PT In vitro identification of genes important for facial skin, useful for
 PT assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.
 XX
 PS Claim 5; SEQ ID NO 1408; 577pp; German.
 XX
 CC This invention describes a novel in vitro method for identifying genes
 CC that are significant for facial skin in humans. The method comprises
 CC recovering, from facial skin, a first mixture of genetically expressed
 CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 CC their fragments), recovering a second, similar mixture from some other
 CC human tissue, preferably skin from a protected area, especially from the
 CC breast and subjecting the mixtures to serial analysis of gene expression
 CC (SAGE) to identify those genes for which expression is markedly different
 CC between facial skin and the other tissue. The invention also describes an
 CC in vitro method for determining homeostasis of human facial skin; a test
 CC kit which comprises a solid support (flexible or rigid) on which are
 CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic
 CC agents. ADO31911-AOQ35111 represent human DNA tag fragments used to

CC identify the facial skin-associated genes described in the invention.

XX Sequence 11 BP; 8 A; 0 C; 2 G; 1 T; 0 U; 0 Other;

SQ Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 619 GAAAGAGAAA 627
|||||
Db 3 GAAAGAGAAA 11

RESULT 109
AA14816
ID AAX14816 standard; DNA; 10 BP.
XX
AC AAX14816;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix forming nucleotides 2103-2112 of Hepatitis B virus.
XX
KW Triple-helix forming region; Triplex formation; DNA detection;
KW identification; bacteria; oncogene; virus; ds.
XX
OS Hepatitis B virus.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-00173489.
XX
PR 29-OCT-1992; 92US-00968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria.
XX
PS Disclosure; Col 19-20; 168pp; English.
XX
CC The present sequence represents a potential triple-helix forming region.
CC It can be used to demonstrate the assay of the invention. The assay
CC comprises adding a sample containing double-stranded DNA test sequences,
CC e.g. containing the present sequence, to an aqueous medium containing at
CC least one complex of anchor DNA, attached to a solid support, and
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC designed to form a triple-strand structure with part of the test
CC sequence. Triplex formation results in displacement of the reporter DNA
CC which is detected as an indication of the presence of the DNA test
CC sequence. The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ Sequence 10 BP; 6 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 618 GGAAGAGAAA 627
|||||
Db 1 GGAAGAGAAA 10

RESULT 111
AA14766/C
ID AAX14766 standard; DNA; 10 BP.
XX
AC AAX14766;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix forming nucleotides 945-954 of Hepatitis B virus.
XX
KW Triple-helix forming region; Triplex formation; DNA detection;
KW identification; bacteria; oncogene; virus; ds.
XX
OS Hepatitis B virus.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-00173489.
XX
PR 29-OCT-1992; 92US-00968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria.
XX
PS Disclosure; Col 19-20; 168pp; English.
XX
CC The present sequence represents a potential triple-helix forming region.
CC It can be used to demonstrate the assay of the invention. The assay
CC comprises adding a sample containing double-stranded DNA test sequences,
CC e.g. containing the present sequence, to an aqueous medium containing at
CC least one complex of anchor DNA, attached to a solid support, and
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC designed to form a triple-strand structure with part of the test
CC sequence. Triplex formation results in displacement of the reporter DNA
CC which is detected as an indication of the presence of the DNA test
CC sequence. The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ Sequence 10 BP; 6 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 618 GGAAGAGAAA 627
|||||
Db 1 GGAAGAGAAA 10

RESULT 110
AA14766/C
ID AAX14766 standard; DNA; 10 BP.
XX
AC AAX14766;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix forming nucleotides 945-954 of Hepatitis B virus.
XX
KW Triple-helix forming region; Triplex formation; DNA detection;
KW identification; bacteria; oncogene; virus; ds.
XX
OS Hepatitis B virus.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-00173489.
XX
PR 29-OCT-1992; 92US-00968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria.
XX
PS Disclosure; Col 19-20; 168pp; English.
XX
CC The present sequence represents a potential triple-helix forming region.
CC It can be used to demonstrate the assay of the invention. The assay
CC comprises adding a sample containing double-stranded DNA test sequences,
CC e.g. containing the present sequence, to an aqueous medium containing at
CC least one complex of anchor DNA, attached to a solid support, and
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC designed to form a triple-strand structure with part of the test
CC sequence. Triplex formation results in displacement of the reporter DNA
CC which is detected as an indication of the presence of the DNA test
CC sequence. The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ Sequence 10 BP; 0 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 618 GGAAGAGAAA 627
|||||
Db 10 GGAAGAGAAA 1

RESULT 111
AA14766/C
ID AAX14766 standard; DNA; 10 BP.
XX
AC AAX14766;
XX
DT 18-MAY-1999 (first entry)
XX
DE WO9904041 Seq ID 6.
XX
KW Melting temperature; Tm; nucleic acid duplex; binding ligand; mismatch;
KW sequencing; hybridisation; binding energy; stringency; ss.

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OS Synthetic.
XX Key Location/Qualifiers
FH misc_binding 1..10
FT /tag= a
FT /note= "Binds to nucleotides 25 to 34 of AAX02954"
XX
FN WO9904041-A1.
XX
XX 28-JAN-1999.
XX
XX 16-JUL-1998; 98WO-US014772.
XX
XX 17-JUL-1997; 97US-0052845P.
XX
XX 16-JUL-1998; 98US-00116393.
XX
XX (TWTE-) TM TECHNOLOGIES INC.
XX
XX Lane MJ, Benight AS, Faldasz BD;
XX
XX WPI; 1999-132281/11.
XX
XX
XX Normalising melting temperatures of different nucleic acid duplexes - by
XX the addition of a ligand that binds in base-preferred manner to modulate
XX duplex stability, particularly for sequencing by hybridisation.
XX
XX Example 4; Page 14; 46pp; English.
XX
XX This invention describes a method for normalising the melting
XX temperatures (Tm) of at least two nucleic acid duplexes by contacting the
XX duplexes with a reaction mixture containing a binding ligand that binds
XX preferentially to one of the duplexes. The binding ligand is used to
XX increase or decrease the differences in Tm between AT- and GC-rich
XX duplexes, particularly in sequencing by hybridisation methods or, by
XX increasing differences in binding energies, to increase stringency and
XX decrease hybridisation of mismatched gene sequences, e.g. in assays for
XX specific targets. By normalising Tm, sequence-dependent differences in
XX binding to a probe are eliminated. This allows accurate sequencing by
XX hybridisation, a method that can potentially provide large amounts of
XX sequence information in a single experiment by using many probes in an
XX array but currently is associated with problems of binding of probes with
XX one or more mismatches
XX
XX Sequence 10 BP; 1 A; 1 C; 0 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 42.0%; Score 8.4; DB 1; Length 10;
XX Best Local Similarity 90.0%; Pred. No. 83;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 620 AAAAGAAAGT 629
XX |||||
XX 10 AAAAAAAGT 1
XX
XX RESULT 112
XX AAZ77678/C
XX ID AAZ77678 standard; DNA; 10 BP.
XX
XX AC AAZ77678;
XX
XX DT 10-APR-2000 (first entry)
XX
XX DE Human dendritic cell SAGE tag, SEQ ID NO:106.
XX
XX KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
XX KW APC; monocyte-derived dendritic cell; differential gene expression;
XX KW immunostimulatory cofactor; costimulatory factor; CTL;
XX KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
XX OS Homo sapiens.
XX
XX FN WO9965924-A2.
XX

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PD 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013800.
XX
XX 19-JUN-1998; 98US-0089833P.
XX
XX 19-JUN-1998; 98US-0089844P.
XX
XX 19-JUN-1998; 98US-0089853P.
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XX 19-JUN-1998; 98US-0089878P.
XX
XX 19-JUN-1998; 98US-0089911P.
XX
XX 19-JUN-1998; 98US-0089932P.
XX
XX 19-JUN-1998; 98US-0089933P.
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XX 19-JUN-1998; 98US-0089934P.
XX
XX 19-JUN-1998; 98US-0089937P.
XX
XX 19-JUN-1998; 98US-0089939P.
XX
XX 19-JUN-1998; 98US-0090000P.
XX
XX 19-JUN-1998; 98US-0090035P.
XX
XX 19-JUN-1998; 98US-0090036P.
XX
XX 19-JUN-1998; 98US-0090039P.
XX
XX 19-JUN-1998; 98US-0090040P.
XX
XX 19-JUN-1998; 98US-0090041P.
XX
XX 19-JUN-1998; 98US-0090042P.
XX
XX 19-JUN-1998; 98US-0090043P.
XX
XX 19-JUN-1998; 98US-0090044P.
XX
XX 19-JUN-1998; 98US-0090045P.
XX
XX 19-JUN-1998; 98US-0090047P.
XX
XX 19-JUN-1998; 98US-0090048P.
XX
XX 19-JUN-1998; 98US-0090072P.
XX
XX 19-JUN-1998; 98US-0090076P.
XX
XX 19-JUN-1998; 98US-0090077P.
XX
XX 19-JUN-1998; 98US-0090078P.
XX
XX 19-JUN-1998; 98US-0090079P.
XX
XX 19-JUN-1998; 98US-0090080P.
XX
XX 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
XX
XX (ROBE/) ROBERTS B L.
XX
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 66; 130pp; English.
XX
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T-cell receptors is alone
XX insufficient to activate a robust cytotoxic immune response that can lyse
XX the tumour cells. Immunostimulatory cofactors also being required for
XX efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX sequences identified using the SAGE tags have several potential uses.
XX They may be used in vaccines to induce an immune response, particularly
XX against a tumour antigen; to modulate the genotype of an APC; to screen
XX for agents that modulate expression of differentially expressed genes in
XX an APC; and as hybridisation probes/amplification primers for the genes
XX diagnosis, prognosis and monitoring of diseases related to abnormal
XX expression of these genes. Detection of the dendritic cell differentially
XX expressed genes, or of their encoded proteins, can be used to identify
XX cells as belonging to the monocyte lineage. Cells containing these genes
XX can be used in active immunotherapy (or to stimulate production of a
XX population of antigen-specific effector cells) and vectors containing

```

CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX Sequence 10 BP; 2 A; 2 C; 0 G; 6 T; 0 U; 0 Other;
 SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 620 AAAGAAAGTG 629
 DB 10 AAAGAAAGTG 1
 RESULT 113
 AAZ78980
 ID AAZ78980 standard; DNA; 10 BP.
 XX
 AC AAZ78980;
 DT 10-APR-2000 (first entry)
 DE Human dendritic cell SAGE tag, SEQ ID NO:1408.
 XX
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965924-A2.
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013800.
 XX
 PR 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-008991P.
 PR 19-JUN-1998; 98US-008992P.
 PR 19-JUN-1998; 98US-008993P.
 PR 19-JUN-1998; 98US-008994P.
 PR 19-JUN-1998; 98US-008997P.
 PR 19-JUN-1998; 98US-008999P.
 PR 19-JUN-1998; 98US-009000P.
 PR 19-JUN-1998; 98US-009003P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106077/09.
 XX
 PT Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 XX
 PS Claim 1; Page 105; 130pp; English.
 XX
 CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 5 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 621 AAAGAAAGTG 630
 DB 1 AAGGAAAGTG 10
 RESULT 114
 AAZ78664/C
 ID AAZ78664 standard; DNA; 10 BP.
 XX
 AC AAZ78664;
 XX
 DT 10-APR-2000 (first entry)
 DE Human dendritic cell SAGE tag, SEQ ID NO:1092.
 XX
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965924-A2.

XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013800.
XX PR 19-JUN-1998; 98US-0089833P.
XX PR 19-JUN-1998; 98US-0089844P.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089878P.
XX PR 19-JUN-1998; 98US-0089911P.
XX PR 19-JUN-1998; 98US-0089922P.
XX PR 19-JUN-1998; 98US-0089933P.
XX PR 19-JUN-1998; 98US-0089944P.
XX PR 19-JUN-1998; 98US-0089977P.
XX PR 19-JUN-1998; 98US-0089999P.
XX PR 19-JUN-1998; 98US-0090000P.
XX PR 19-JUN-1998; 98US-0090035P.
XX PR 19-JUN-1998; 98US-0090036P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PR 19-JUN-1998; 98US-0090042P.
XX PR 19-JUN-1998; 98US-0090043P.
XX PR 19-JUN-1998; 98US-0090044P.
XX PR 19-JUN-1998; 98US-0090045P.
XX PR 19-JUN-1998; 98US-0090047P.
XX PR 19-JUN-1998; 98US-0090048P.
XX PR 19-JUN-1998; 98US-0090072P.
XX PR 19-JUN-1998; 98US-0090076P.
XX PR 19-JUN-1998; 98US-0090077P.
XX PR 19-JUN-1998; 98US-0090078P.
XX PR 19-JUN-1998; 98US-0090079P.
XX PR 19-JUN-1998; 98US-0090080P.
XX PR 08-DEC-1998; 98US-0111715P.
XX PA (GENZ) GENZYME CORP.
XX FA (ROBEY) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPT; 2000-106077/09.
XX PT Isolated polynucleotides differentially expressed in antigen-presenting
XX PT cells, useful in gene vaccines against cancer.
XX PS Claim 1; Page 96; 130pp; English.
XX CC Sequences AAZ7573-279709 represent SAGE (serial analysis of gene
XX CC expression) tags used to identify mRNA transcripts encoding
XX CC immunostimulatory cofactor proteins which are preferentially or
XX CC differentially expressed in monocyte-derived dendritic cells compared
XX CC with monocytes. Some of the transcripts correspond to known genes or ESTs
XX CC (expressed sequence tags) which were previously unknown to be
XX CC preferentially or differentially expressed in dendritic cells, while
XX CC other transcripts correspond to novel genes. Antigen-presenting cell
XX CC (APC)-associated costimulatory factors play an important role in the
XX CC activation of the cytotoxic immune response, particularly against tumour
XX CC cells. Tumour antigen presentation via the MHC (major histocompatibility
XX CC complex) and subsequent recognition by T-cell receptors is alone
XX CC insufficient to activate a robust cytotoxic immune response that can lyse
XX CC the tumour cells, immunostimulatory cofactors also being required for
XX CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX CC sequences identified using the SAGE tags have several potential uses.
XX CC They may be used in vaccines to induce an immune response, particularly
XX CC against a tumour antigen; to modulate the genotype of an APC; to screen
XX CC for agents that modulate expression of differentially expressed genes in
XX CC an APC; and as hybridisation probes/amplification primers for the
XX CC diagnosis, prognosis and monitoring of diseases related to abnormal
XX CC expression of these genes. Detection of the dendritic cell differentially
XX CC expressed genes, or of their encoded proteins, can be used to identify
XX CC cells as belonging to the monocyte lineage. Cells containing these genes
XX CC can be used in active immunotherapy for to stimulate production of a

CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 623 AGAAAGTGCT 632
|||||
DB 10 AGAATGTGCT 1
RESULT 115
AAZ78219
ID AAZ78219 standard; DNA; 10 BP.
XX
AC AAZ78219;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:647.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
FN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
XX PR 19-JUN-1998; 98US-0089844P.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089878P.
XX PR 19-JUN-1998; 98US-0089911P.
XX PR 19-JUN-1998; 98US-0089922P.
XX PR 19-JUN-1998; 98US-0089933P.
XX PR 19-JUN-1998; 98US-0089944P.
XX PR 19-JUN-1998; 98US-0089977P.
XX PR 19-JUN-1998; 98US-0089999P.
XX PR 19-JUN-1998; 98US-0090000P.
XX PR 19-JUN-1998; 98US-0090035P.
XX PR 19-JUN-1998; 98US-0090036P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PR 19-JUN-1998; 98US-0090042P.
XX PR 19-JUN-1998; 98US-0090043P.
XX PR 19-JUN-1998; 98US-0090044P.
XX PR 19-JUN-1998; 98US-0090045P.
XX PR 19-JUN-1998; 98US-0090047P.
XX PR 19-JUN-1998; 98US-0090048P.
XX PR 19-JUN-1998; 98US-0090072P.
XX PR 19-JUN-1998; 98US-0090076P.
XX PR 19-JUN-1998; 98US-0090077P.
XX PR 19-JUN-1998; 98US-0090078P.
XX PR 19-JUN-1998; 98US-0090079P.
XX PR 19-JUN-1998; 98US-0090080P.
XX PR 08-DEC-1998; 98US-0111715P.
XX PA (GENZ) GENZYME CORP.

PA	(ROBE//) ROBERTS B L.
RA	(SHAN//) SHANKARA S.
XX	
PI	Roberts BL, Shankara S;
XX	
DR	WPI; 2000-106077/09.
XX	
PT	Isolated polynucleotides differentially expressed in antigen-presenting
PT	cells, useful in gene vaccines against cancer.
XX	
PS	Claim 1; Page 84; 130pp; English.
XX	
CC	Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC	expression) tags used to identify mRNA transcripts encoding
CC	immunostimulatory cofactor proteins which are preferentially or
CC	differentially expressed in monocyte-derived dendritic cells compared
CC	with monocytes. Some of the transcripts correspond to known genes or ESTs
CC	(expressed sequence tags) which were previously unknown to be
CC	preferentially or differentially expressed in dendritic cells, while
CC	other transcripts correspond to novel genes. Antigen-presenting cell
CC	(APC)-associated costimulatory factors play an important role in the
CC	activation of the cytotoxic immune response, particularly against tumour
CC	cells. Tumour antigen presentation via the MHC (major histocompatibility
CC	complex) and subsequent recognition by T-cell receptors is alone
CC	insufficient to activate a robust cytotoxic immune response that can lyse
CC	the tumour cells, immunostimulatory cofactors also being required for
CC	efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC	sequences identified using the SAGE tags have several potential uses.
CC	They may be used in vaccines to induce an immune response, particularly
CC	against a tumour antigen; to modulate the genotype of an APC; to screen
CC	for agents that modulate expression of differentially expressed genes in
CC	an APC; and as hybridisation probes/amplification primers for the
CC	diagnosis, prognosis and monitoring of diseases related to abnormal
CC	expression of these genes. Detection of the dendritic cell differentially
CC	expressed genes, or of their encoded proteins, can be used to identify
CC	cells as belonging to the monocyte lineage. Cells containing these genes
CC	can be used in active immunotherapy (or to stimulate production of a
CC	population of antigen-specific effector cells) and vectors containing
CC	them are used in gene therapy. Co-administration of tumour antigens and
CC	APC-associated costimulatory factors ensures adequate antigen
CC	presentation to endogenous APCs and upregulates the APCs for the
CC	presentation of co-stimulatory signals, migration to T cell-rich sites,
CC	secretion of T cell growth factors and secretion of chemokines for
CC	recruitment of immune effector cells
XX	
SQ	Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;
	Query Match 42.0%; Score 8.4; DB 1; Length 10;
	Best Local Similarity 90.0%; Pred. No. 83;
	Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	617 CGGAAAGAA 626
Db	1 CGGAAAGAA 10
RESULT 116	
AZB3766	
ID	AZB3766 standard; DNA; 10 BP.
XX	
AC	AZB3766;
XX	
DT	07-APR-2000 (first entry)
XX	
DE	Metastatic breast tumour cell upregulated transcript tag #3000.
XX	
KW	Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW	non-metastatic breast tumour tissue; gene therapy; anticancer;
XX	antimetastatic; vaccine; diagnosis; ss.
OS	Homo sapiens.
PX	
PN	WO9965928-A2.

XX	23-DEC-1999.
PD	
XX	
PF	
XX	18-JUN-1999; 99WO-US013647.
XX	
PR	19-JUN-1998; 98US-0089853P.
PR	19-JUN-1998; 98US-0089997P.
PR	19-JUN-1998; 98US-0090039P.
PR	19-JUN-1998; 98US-0090040P.
PR	19-JUN-1998; 98US-0090041P.
XX	(GENZ) GENZYME CORP.
PA	(ROBE/) ROBERTS B L.
PA	(SHAN/) SHANKARA S.
XX	
PI	Roberts BL, Shankara S;
XX	
DR	WPI; 2000-106079/09.
XX	
PT	Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
PT	
XX	
PS	Claim 1; Page 139; 219pp; English.
XX	
CC	AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences).
CC	Particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy
XX	
SC	Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
	Query Match 42.0%; Score 8.4; DB 1; Length 10;
	Best Local Similarity 90.0%; Pred. No. 83;
	Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0
OY	625 AAAGTGTGG 634
Db.	1 AAGTGCTGG 10
	RESULT 117
ID	AAZ83450
XX	ID AAZ83450 standard; DNA; 10 BP.
XX	
AC	AAZ83450;
XX	
DT	07-APR-2000 (first entry)
XX	
DE	Metastatic breast tumour cell upregulated transcript tag #2694.
XX	
KW	Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW	non-metastatic breast tumour tissue; gene therapy; anticancer;
KW	antimetastatic; vaccine; diagnosis; ss.
OS	Homo sapiens.

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XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 131; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
    Query Match 42.0%; Score 8.4; DB 1; Length 10;
    Best Local Similarity 90.0%; Pred. No. 83;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 617 CGGAAGAAGAA 626
DB 1 CGGAAGAAAAA 10
RESULT 118
AAZ81243
ID AAZ81243 standard; DNA; 10 BP.
XX AC AAZ81243;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #477.
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; Gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.

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XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 71; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 7 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
    Query Match 42.0%; Score 8.4; DB 1; Length 10;
    Best Local Similarity 90.0%; Pred. No. 83;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 620 AAAAGAAAGT 629
DB 1 AAAAGAAACT 10
RESULT 119
AAZ81950
ID AAZ81950 standard; DNA; 10 BP.
XX AC AAZ81950;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #1184.
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW antimetastatic; vaccine; diagnosis; ss.

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KW	non-metastatic breast tumour tissue; gene therapy; anticancer;
KW	antimetastatic; vaccine; diagnosis; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO9965928-A2.
XX	
PD	23-DEC-1999.
XX	
PF	18-JUN-1999; 99WO-US013647.
XX	
PR	19-JUN-1998; 98US-0089853P.
PR	19-JUN-1998; 98US-0089997P.
PR	19-JUN-1998; 98US-0090039P.
PR	19-JUN-1998; 98US-0090040P.
PR	19-JUN-1998; 98US-0090041P.
XX	
PA	(GENZ) GENZYME CORP.
PA	(ROBE/) ROBERTS B L.
PA	(SHAN/) SHANKARA S.
XX	
PI	Roberts BL, Shankara S;
XX	
DR	WPI; 2000-106079/09.
XX	
PT	Isolated polynucleotides differentially expressed between metastatic and
PT	non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT	treatment of cancer.
XX	
PS	Claim 1; Page 90; 219pp; English.
XX	
CC	AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC	that are preferentially transcribed in the metastatic breast tumour
CC	tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC	to AAZ86677 represent tags corresponding to distinct transcripts that are
CC	preferentially transcribed in the primary or non-metastatic breast tumour
CC	tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC	transcripts can be used for diagnosis, prognosis, monitoring and
CC	treatment of breast cancer, particularly where metastatic. Diagnosis is
CC	by standard immunoassays or hybridisation/amplification reactions.
CC	Compounds that modulate expression of the transcripts are potentially
CC	useful for treatment of (metastatic) breast cancer, while promoters from
CC	e.g. therapeutic genes (also ribozymes or antisense sequences),
CC	particularly an antigen-encoding sequence for use in gene or cell-based
CC	vaccines. Polypeptides encoded by the transcripts are also useful in
CC	antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC	agents. Host cells that produce the polypeptides can be used to expand
CC	and isolate populations of educated, antigen-specific immune effector
CC	cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC	immunotherapy
XX	
SQ	Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
	Query Match 42.0%; Score 8.4; DB 1; Length 10;
	Best Local Similarity 90.0%; Pred. No. 83;
	Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	619 GAAACGAAG 628
Db	1 GAAACGAAG 10
	RESULT 120
AAZ83641	
ID	AAZ83641 standard; DNA; 10 BP.
XX	
AC	AAZ83641;
XX	
DT	07-APR-2000 (first entry)
XX	
DE	Metastatic breast tumour cell upregulated transcript tag #2875.

XX	Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW	non-metastatic breast tumour tissue; gene therapy; anticancer;
KW	antimetastatic; vaccine; diagnosis; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO9965928-A2.
XX	
PD	23-DEC-1999.
XX	
PF	18-JUN-1999; 99WO-US013647.
XX	
PR	19-JUN-1998; 98US-0089853P.
PR	19-JUN-1998; 98US-0089997P.
PR	19-JUN-1998; 98US-0090039P.
PR	19-JUN-1998; 98US-0090040P.
PR	19-JUN-1998; 98US-0090041P.
XX	
PA	(GENZ) GENZYME CORP.
PA	(ROBE/) ROBERTS B L.
PA	(SHAN/) SHANKARA S.
XX	
PI	Roberts BL, Shankara S;
XX	
DR	WPI; 2000-106079/09.
XX	
PT	Isolated polynucleotides differentially expressed between metastatic and
PT	non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT	treatment of cancer.
XX	
PS	Claim 1; Page 136; 219pp; English.
XX	
CC	AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC	that are preferentially transcribed in the metastatic breast tumour
CC	tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC	to AAZ86677 represent tags corresponding to distinct transcripts that are
CC	preferentially transcribed in the primary or non-metastatic breast tumour
CC	tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC	transcripts can be used for diagnosis, prognosis, monitoring and
CC	treatment of breast cancer, particularly where metastatic. Diagnosis is
CC	by standard immunoassays or hybridisation/amplification reactions.
CC	Compounds that modulate expression of the transcripts are potentially
CC	useful for treatment of (metastatic) breast cancer, while promoters from
CC	e.g. therapeutic genes (also ribozymes or antisense sequences),
CC	particularly an antigen-encoding sequence for use in gene or cell-based
CC	vaccines. Polypeptides encoded by the transcripts are also useful in
CC	antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC	agents. Host cells that produce the polypeptides can be used to expand
CC	and isolate populations of educated, antigen-specific immune effector
CC	cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC	immunotherapy
XX	
SQ	Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
	Query Match 42.0%; Score 8.4; DB 1; Length 10;
	Best Local Similarity 90.0%; Pred. No. 83;
	Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	624 GAAAGTCTG 633
Db	1 GAAAGTCTG 10
	RESULT 121
AAZ83175	
ID	AAZ83175 standard; DNA; 10 BP.
XX	
AC	AAZ83175;
XX	
DT	07-APR-2000 (first entry)
XX	
DE	Metastatic breast tumour cell upregulated transcript tag #2875.

XX DE Metastatic breast tumour cell upregulated transcript tag #2409.
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX DR Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX PS Claim 1; Page 124; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
SQ Sequence 10 BP; 6 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 620 AAAGGAAGT 629
Db 1 AAAGGAAGT 10
RESULT 122
AAZ81051/c
ID AAZ81051 standard; DNA; 10 BP.
XX AC AAZ81051;

XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #285.
XX DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX DR Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX PS Claim 1; Page 65; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
SQ Sequence 10 BP; 2 A; 2 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 620 AAAGGAAGT 629
Db 10 AAAGGAAGT 1
RESULT 123
AAZ84388
ID AAZ84388 standard; DNA; 10 BP.

```
XX AC AAZ84388;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #3622.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX KW Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 155; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 621 AAGAGAAAGTG 630
DB 1 AAGACAGTG 10
RESULT 124
```

```
AAZ85130
ID AAZ85130 standard; DNA; 10 BP.
XX AC AAZ85130;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #4364.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX DR WPI; 2000-106079/09.
XX KW Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 176; 219pp; English.
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector
XX CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX CC immunotherapy
XX SQ Sequence 10 BP; 8 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 618 GGAAGAGAAA 627
DB 1 GGAAGAGAAA 10
```

RESULT 125
AAZ81581
ID AAZ81581 standard; DNA; 10 BP.
XX
AC AAZ81581;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #815.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN W09965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090033P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 80; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab) Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 624 GAAAGTGTCTG 633
|||||

Db 1 GAAAGAGCTG 10
RESULT 126
AAC74107/c
ID AAC74107 standard; cDNA; 10 BP.
XX
AC AAC74107;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human dendritic cell and monocyte expressed gene oligonucleotide #194.
XX
KW Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
KW autoimmune disease; tumour; ss.
XX
OS Homo sapiens.
XX
PN W0200060074-A1.
XX
PD 12-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-JP002019.
XX
PR 01-APR-1999; 99JP-00095481.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Hashimoto S, Matsushima K, Suzuki T;
XX
DR WPI; 2000-619172/59.
XX
PT Groups of genes expressed in human dendritic cells at a greater or lesser
PT extent than in monocytes for investigation and diagnosis of autoimmune
PT disease and tumors.
XX
PS Claim 10; Page 13; 95pp; Japanese.
XX
CC The present invention describes a group of genes consisting of 100 genes
CC which are highly expressed in human dendritic cells; a group of genes
CC which are expressed at a higher frequency in human dendritic cells than
CC in human monocytes; and a group of genes which are expressed at lower
CC frequency in human dendritic cells than in human monocytes. Each group of
CC genes are characterised in that cDNAs of these genes respectively have
CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
CC to AAC74213), each is continuous with the base sequence 5'-CATG-3',
CC located most closely to the poly-A region. The sequences can be used for
CC the investigation of the role and mechanism of the involvement of
CC dendritic cells in the immune system and for the study and diagnosis of
CC diseases in which dendritic cells play a significant role, e.g. cancers
CC and autoimmune diseases
XX
SQ Sequence 10 BP; 2 A; 2 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 620 AAAAGAAAGT 629
|||||
Db 10 AAAAGAAAGT 1
RESULT 127
AAA56494/c
ID AAA56494 standard; DNA; 10 BP.
XX
AC AAA56494;
XX
DT 07-SEP-2000 (first entry)
XX
DE Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:388.

```
XX Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
KW granulocyte-macrophage colony-stimulating factor; characterisation;
KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
KW disease onset mechanism; genetic disease; drug development; ss.
XX
OS Homo sapiens.
XX
XX WO200024892-A1.
XX
XX 04-MAY-2000.
XX
XX 28-OCT-1999; 99WO-JP005982.
XX
XX 28-OCT-1998; 98JP-00307532.
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
XX Hashimoto S, Matsuhashima K, Suzuki T;
XX
XX WPI; 2000-350734/30.
XX
XX Genes most frequently expressed in human monocytes and GM-macrophages and
XX M-macrophages studied and with cDNAs characterized, for study of gene
XX specificity, disease onset mechanism, drug development and diagnosis.
XX
XX Claim 31; Page 116; 138pp; Japanese.
XX
XX The present invention describes 100 human genes, which are expressed most
XX frequently in human monocytes. The cDNA of each gene has a sequence fully
XX defined in the specification, and lacking the CATG sequence located
XX adjacent to polyA region. Also described are: (1) an antibody
XX specifically for the protein encoded by any of the genes; (2)
XX oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
XX from human monocytes by granulocyte-macrophage colony-stimulating factor,
XX which are expressed most frequently in human macrophages, differentiated
XX the cDNA of each gene has a fully defined sequence, given in the
XX specification, lacking the base sequence CATG located most closely to the
XX poly A region; (4) an antibody specifically for the protein encoded by
XX sequences of (3). The genes and cDNAs, are used for the study of gene
XX specificity and disease onset mechanism e.g. oncogenesis, genetic
XX diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
XX specifically claimed oligonucleotide tag sequences for human genes
XX expressed in monocytes and macrophages
XX
XX Sequence 10 BP; 2 A; 2 C; 0 G; 6 T; 0 U; 0 Other;
SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 620 AAAAGAAAGT 629
DB 10 AAAAGAAAGT 1
RESULT 128
AAA56419/C
ID AAA56419 standard; DNA; 10 BP.
XX
XX AAA56419;
XX
XX 07-SEP-2000 (first entry)
XX
XX Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:313.
XX
XX Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
XX granulocyte-macrophage colony-stimulating factor; characterisation;
XX GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
XX disease onset mechanism; genetic disease; drug development; ss.
XX
XX Homo sapiens.
XX
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XX WO200024892-A1.
XX
XX 04-MAY-2000.
XX
XX 28-OCT-1999; 99WO-JP005982.
XX
XX 28-OCT-1998; 98JP-00307532.
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
XX Hashimoto S, Matsuhashima K, Suzuki T;
XX
XX WPI; 2000-350734/30.
XX
XX Genes most frequently expressed in human monocytes and GM-macrophages and
XX M-macrophages studied and with cDNAs characterized, for study of gene
XX specificity, disease onset mechanism, drug development and diagnosis.
XX
XX Claim 19; Page 101; 138pp; Japanese.
XX
XX The present invention describes 100 human genes, which are expressed most
XX frequently in human monocytes. The cDNA of each gene has a sequence fully
XX defined in the specification, and lacking the CATG sequence located
XX adjacent to polyA region. Also described are: (1) an antibody
XX specifically for the protein encoded by any of the genes; (2)
XX oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
XX from human monocytes by granulocyte-macrophage colony-stimulating factor,
XX which are expressed most frequently in human macrophages, differentiated
XX the cDNA of each gene has a fully defined sequence, given in the
XX specification, lacking the base sequence CATG located most closely to the
XX poly A region; (4) an antibody specifically for the protein encoded by
XX sequences of (3). The genes and cDNAs, are used for the study of gene
XX specificity and disease onset mechanism e.g. oncogenesis, genetic
XX diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
XX specifically claimed oligonucleotide tag sequences for human genes
XX expressed in monocytes and macrophages
XX
XX Sequence 10 BP; 2 A; 2 C; 0 G; 6 T; 0 U; 0 Other;
SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 620 AAAAGAAAGT 629
DB 10 AAAAGAAAGT 1
RESULT 129
AAH63756
ID AAH63756 standard; cDNA; 10 BP.
XX
XX AAH63756;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 596.
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
XX
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX
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PA (UYJO ) UNIV JOHNS HOPKINS.
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptsomes expressed in particular
PT cell types.
XX
XX Claim 13; Page 52; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptsomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptsomes described in the exemplification of the invention
XX
XX Sequence 10 BP; 8 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
SQ
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 618 GGAAGAGAAA 627
Db 1 GGAAGAGAAA 10
RESULT 130
AAH64268
ID AAH64268 standard; cDNA; 10 BP.
XX
XX AAH64268;
AC
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1108.
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
XX
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptsomes expressed in particular
PT cell types.
XX
XX Claim 13; Page 52; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptsomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptsomes described in the exemplification of the invention
XX
XX Sequence 10 BP; 8 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
SQ
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 618 GGAAGAGAAA 627
Db 1 GGAAGAGAAA 10
RESULT 132
AAH64268
ID AAH64268 standard; cDNA; 10 BP.
XX
XX
```

function of a diseased cell or tissue. The present sequence is one of the transcriptsomes described in the exemplification of the invention

Sequence 10 BP; 7 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 83; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAAGAAAGT 629
|||||||
1 AAAAGAAAGT 10

RESULT 131
AAH63755
ID AAH63755 standard; cDNA; 10 BP.

XX
XX AAH63755;
AC
XX
XX 20-SEP-2001 (first entry)
XX
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 595.
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
XX
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI
XX
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptsomes expressed in particular cell types.
XX
XX Claim 13; Page 52; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161- AAH64724 is expressed by the cell. The transcriptsomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptsomes described in the exemplification of the invention

Sequence 10 BP; 8 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 83; Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAGAAA 627
|||||||
1 GGAAGAGAAA 10

RESULT 132
AAH64268
ID AAH64268 standard; cDNA; 10 BP.

XX

AC AAF98126;
 XX 19-JUN-2001 (first entry)
 XX Human IGRA gene polymorphism detection primer SEQ ID NO:165.
 DE Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGRA;
 KW single nucleotide polymorphism; SNP; allele specific oligonucleotide;
 KW immunoassay; detection; PCR primer; probe; ss.
 OS Homo sapiens.
 XX WO200111010-A2.
 PN 15-FEB-2001.
 XX 02-AUG-2000; 2000WO-US021097.
 PF 09-AUG-1999; 99US-0147860P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Chew A, Denton RR, Duda A, Kliem SE, Lanz EM, Nandabalan K;
 PI Stephens JC;
 PI WPI; 2001-202766/20.
 DR New polynucleotide for gene therapy, comprises nucleotide polymorphisms
 PT in the immunoglobulin E receptor I alpha subunit gene.
 XX Disclosure; Page 24; 99pp; English.
 PS The present invention describes an isolated polynucleotide (I) comprising
 CC a nucleotide sequence (S) which is a polymorphic variant of a reference
 CC sequence for the human immunoglobulin E receptor I alpha subunit (IGRA)
 CC gene or its fragment. The polymorphic variant comprises at least one
 CC polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,
 CC PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine
 CC (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at
 CC PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide
 CC 251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at
 CC a position corresponding to nucleotide 530. (I) can be used in gene
 CC therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
 CC encoded by (I) is useful in drug screening assays and in assays to
 CC measure the binding affinity of one or more candidate drugs targeting
 CC (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
 CC solution and also reacts with (II) on Western or immunoblots of
 CC polyacrylamide gels on membrane supports or substrates. (III) is also
 CC useful in immunoassays to detect (II) in biological samples. AAF97965 to
 CC AAF98096 represent IGRA allele specific oligonucleotide probes; AAF98097
 CC to AAF98140 represent IGRA gene polymorphism detection primers; and
 CC AAF98141 to AAF98180 represent IGRA gene PCR primers which are used in
 CC the exemplification of the present invention
 XX Sequence 10 BP; 6 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
 SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 619 GAAAGAAAG 628
 DB |||||
 1 GAAAGAGAG 10
 RESULT 133
 AAH32738/c
 ID AAH32738 standard; cDNA; 10 BP.
 XX AC AAH32738;
 XX DT 13-AUG-2001 (first entry)
 XX (UYJO) UNIV JOHNS HOPKINS.

DE LPS activated human monocyte expression gene cDNA tag SEQ:111.
 XX Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
 KW expressed sequence tag; diagnosis; human disease; treatment; ss.
 OS Homo sapiens.
 XX JP2001069993-A.
 PN 21-MAR-2001.
 PD 28-APR-2000; 2000JP-00131079.
 PF 08-JUL-1999; 99JP-00195103.
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2001-304369/32.
 DR LPS activated human monocyte expression gene group.
 XX Claim 10; Page 25; 52pp; Japanese.
 PS The present invention describes a lipopolysaccharide (LPS) activated
 CC human monocyte expression gene group consisting of the high-ranking 50
 CC genes of the highest expression among the genes expressed by human
 CC monocyte stimulated by LPS in which the cDNA of each gene has the base
 CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
 CC CATG-3' nearest to the polyA region. The gene group is useful for the
 CC development of new means for the diagnosis and the treatment of various
 CC human diseases in which human monocyte plays an important role. AAH32628
 CC to AAH32943 represent specifically claimed LPS activated human monocyte
 CC expression gene cDNA tags from the present invention. AAH32944 represents
 CC an LPS activated human monocyte expression gene cDNA sequence encoding
 CC AA98009, which are given in the exemplification of the present invention
 XX Sequence 10 BP; 2 A; 2 C; 0 G; 6 T; 0 U; 0 Other;
 SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 620 AAAAGAAAGT 629
 DB |||||
 10 AAAAGAAATGT 1
 RESULT 134
 AAF33775/c
 ID AAF33775 standard; DNA; 10 BP.
 XX AC AAF33775;
 XX DT 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:514.
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 OS WO200077214-A2.
 PN 21-DEC-2000.
 PD 14-JUN-2000; 2000WO-US016223.
 PF 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Claim 1; Page 393; 419pp; English.
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
 SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 620 AAAAGAACT 629
 |||||
 Db 10 AAAAGAACT 1
 RESULT 135
 AAF33616
 ID AAF33616 standard; DNA; 10 BP.
 XX AAF33616;
 AC AAF33616;
 XX 23-MAR-2001 (first entry)
 DT 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:355.
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 OS Saccharomyces cerevisiae.
 XX WO200077214-A2.
 PN WO200077214-A2.
 XX 21-DEC-2000.
 PD 21-DEC-2000.
 XX 14-JUN-2000; 2000WO-US016223.

PR 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Claim 1; Page 387; 419pp; English.
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 624 GAAAGTGCTG 633
 |||||
 Db 1 GAAAGTGATG 10
 RESULT 136
 AAF34158/C
 ID AAF34158 standard; DNA; 10 BP.
 XX AAF34158;
 AC AAF34158;
 XX 23-MAR-2001 (first entry)
 DT 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:897.
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 OS Saccharomyces cerevisiae.
 XX WO200077214-A2.
 PN WO200077214-A2.
 XX 21-DEC-2000.
 PD 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.
 XX 21-DEC-2000.
 XX 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX gene expression (SAGE) tags, useful for studying, monitoring and
 XX affecting phases of the cell cycle.
 XX Example; Page 32; 419pp; English.
 XX The present invention describes an isolated DNA molecule comprising a
 XX coding sequence of a yeast gene selected from a group of 745 NORF (not
 XX previously assigned open reading frame; or nonannotated ORF) genes
 XX comprising a SAGE (serial analysis of gene expression) tag. Also
 XX described are: (1) a method (M1) of using NORF genes to affect the cell
 XX cycle comprising administering a NORF gene whose expression varies by at
 XX least 10% between any two phases of the cell cycle selected from log
 XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
 XX antifungal drugs comprising: (a) contacting a test substance with a yeast
 XX cell; and (b) monitoring expression of a NORF gene whose expression
 XX varies as in M1, where a test substance which modifies the expression of
 XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 XX identifying human genes which are involved in cell cycle progression
 XX comprising contacting human DNA with a probe which comprises at least 10
 XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
 XX and (4) a method (M4) for identifying a candidate drug as a member of a
 XX class of drugs having a characteristic effect on gene expression in a
 XX yeast cell comprising contacting a yeast cell with a candidate drug and
 XX monitoring expression in the yeast cell of at least 1 NORF gene whose
 XX expression is affected by the class of drugs. The NORF genes may be used
 XX to study, monitor and affect phases of the cell cycle, the differentially
 XX expressed genes may be used as markers of phases of the cell cycle. The
 XX methods may be used to identify candidate drugs which affect the cell
 XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 XX represent SAGE tags used in the exemplification of the present invention.
 XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 XX method, in the exemplification of the present invention
 XX Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
 XX Query Match 42.0%; Score 8.4; DB 1; Length 10;
 XX Best Local Similarity 90.0%; Pred. No. 83;
 XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 620 AAAAGAACT 629
 Db 10 AAAAGAACGT 1
 RESULT 137
 AAF38587
 ID AAF38587 standard; DNA; 10 BP.
 XX AAF38587;
 XX 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5326.
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
 XX serial analysis of gene expression; antifungal; tag; identification;
 XX linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.

PN WO200077214-A2.
 XX 21-DEC-2000.
 XX 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX gene expression (SAGE) tags, useful for studying, monitoring and
 XX affecting phases of the cell cycle.
 XX Example; Page 190; 419pp; English.
 XX The present invention describes an isolated DNA molecule comprising a
 XX coding sequence of a yeast gene selected from a group of 745 NORF (not
 XX previously assigned open reading frame; or nonannotated ORF) genes
 XX comprising a SAGE (serial analysis of gene expression) tag. Also
 XX described are: (1) a method (M1) of using NORF genes to affect the cell
 XX cycle comprising administering a NORF gene whose expression varies by at
 XX least 10% between any two phases of the cell cycle selected from log
 XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
 XX antifungal drugs comprising: (a) contacting a test substance with a yeast
 XX cell; and (b) monitoring expression of a NORF gene whose expression
 XX varies as in M1, where a test substance which modifies the expression of
 XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 XX identifying human genes which are involved in cell cycle progression
 XX comprising contacting human DNA with a probe which comprises at least 10
 XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
 XX and (4) a method (M4) for identifying a candidate drug as a member of a
 XX class of drugs having a characteristic effect on gene expression in a
 XX yeast cell comprising contacting a yeast cell with a candidate drug and
 XX monitoring expression in the yeast cell of at least 1 NORF gene whose
 XX expression is affected by the class of drugs. The NORF genes may be used
 XX to study, monitor and affect phases of the cell cycle, the differentially
 XX expressed genes may be used as markers of phases of the cell cycle. The
 XX methods may be used to identify candidate drugs which affect the cell
 XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 XX represent SAGE tags used in the exemplification of the present invention.
 XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 XX method, in the exemplification of the present invention
 XX Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
 XX Query Match 42.0%; Score 8.4; DB 1; Length 10;
 XX Best Local Similarity 90.0%; Pred. No. 83;
 XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 625 AAAGTGCTGG 634
 Db 1 AAAGTGCTGG 10
 RESULT 138
 AAF36214
 ID AAF36214 standard; DNA; 10 BP.
 XX AAF36214;
 XX 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2953.
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 XX nor previously assigned open reading frame; nonannotated ORF; SAGE;
 XX serial analysis of gene expression; antifungal; tag; identification;
 XX linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.
 XX PN WO200077214-A2.
 XX PD 21-DEC-2000.
 XX PF 14-JUN-2000; 2000WO-US016223.
 XX PR 16-JUN-1999; 99US-00335032.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Velulescu V, Vogelstein B, Kinzler K;
 XX DR WPI; 2001-061874/07.
 XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX PS Example; Page 105; 419pp; English.
 XX CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 625 AAAGTGCTGG 634
 | | | | | | | | | |
 Db 1 ACAGTGCTGG 10
 RESULT 139
 AAF33615
 ID AAF33615 standard; DNA; 10 BP.
 XX AC AAF33615;
 XX 23-MAR-2001 (first entry)
 XX DT
 XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:354.
 XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX OS Saccharomyces cerevisiae.
 XX PN WO200077214-A2.
 XX PD 21-DEC-2000.
 XX PF 14-JUN-2000; 2000WO-US016223.
 XX PR 16-JUN-1999; 99US-00335032.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Velulescu V, Vogelstein B, Kinzler K;
 XX DR WPI; 2001-061874/07.
 XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX PS Claim 1; Page 387; 419pp; English.
 XX CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX SQ Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 624 GAAAGTGCTG 633
 | | | | | | | | | |
 Db 1 GAAAGTGATG 10
 RESULT 140
 AAF40411/C
 ID AAF40411 standard; DNA; 10 BP.
 XX AC AAF40411;
 XX 23-MAR-2001 (first entry)
 XX DT
 XX KW

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7150.
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 255; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX Sequence 10 BP; 1 A; 1 C; 0 G; 8 T; 0 U; 0 Other;
SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 620 AAAGAAAGT 629
Db 10 AAAGAAAGT 1
RESULT 141
AAF38491
ID AAF38491 standard; DNA; 10 BP.
XX
AC AAF38491;

XX 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5230.
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
XX 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 186; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX Sequence 10 BP; 6 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
SQ Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 621 AAAGAAAGT 630
Db 1 AAAGAAAGT 10
RESULT 142
AAF35093

ID AAF35093 standard; DNA; 10 BP.
 AC AAF35093;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1832.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 DR
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 65; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 624 GAAAGTGCTG 633
 DB |||||
 1 GAAAGTGATG 10

RESULT 143
 AAF43945/C
 ID AAF43945 standard; DNA; 10 BP.
 XX
 AC AAF43945;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:12084.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velulescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 DR
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 381; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 618 GGAAAGAGAA 627

	Matches	9;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	620	AAAGAAAGT	629							
Db	1	AATAGAAAGT	10							
RESULT 145										
AAF39649/C										
ID	AAF39649	standard; DNA; 10 BP.								
XX	AC	AAF39649;								
XX	AC									
XX	AC									
DT	23-MAR-2001	(first entry)								
XX	XX									
DE	Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6388.									
XX	XX									
KW	Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;									
KW	nor previously assigned open reading frame; nonannotated ORF; SAGE;									
KW	serial analysis of gene expression; antifungal; tag; identification;									
KW	linker; PCR primer; ds.									
XX	XX									
OS	Saccharomyces cerevisiae.									
XX	XX									
PN	WO200077214-A2.									
PD	21-DEC-2000.									
XX	XX									
PF	14-JUN-2000; 2000WO-US016223.									
XX	XX									
PR	16-JUN-1999; 99US-00335032.									
XX	XX									
PA	(UYJO) UNIV JOHNS HOPKINS.									
XX	XX									
PI	Velculescu V, Vogelstein B, Kinzler K;									
XX	XX									
DR	WPI; 2001-061874/07.									
XX	XX									
PT	Yeast gene coding sequences comprising NORF genes with serial analysis of									
PT	gene expression (SAGE) tags, useful for studying, monitoring and									
PT	affecting phases of the cell cycle.									
XX	XX									
PS	Example; Page 204; 419pp; English.									
XX	XX									
CC	The present invention describes an isolated DNA molecule comprising a									
CC	coding sequence of a yeast gene selected from a group of 745 NORF (not									
CC	previously assigned open reading frame; or nonannotated ORF) genes									
CC	comprising a SAGE (serial analysis of gene expression) tag. Also									
CC	described are: (1) a method (M1) of using NORF genes to affect the cell									
CC	cycle comprising administering a NORF gene whose expression varies by at									
CC	least 10% between any two phases of the cell cycle selected from log									
CC	phase, S phase and G2/M; (2) a method (M2) for screening candidate									
CC	antifungal drugs comprising: (a) contacting a test substance with a yeast									
CC	cell; and (b) monitoring expression of a NORF gene whose expression									
CC	varies as in M1, where a test substance which modifies the expression of									
CC	the yeast gene is a candidate antifungal drug; (3) a method (M3) for									
CC	identifying human genes which are involved in cell cycle progression									
CC	comprising contacting human DNA with a probe which comprises at least 10									
CC	contiguous nucleotides of a NORF gene whose expression varies as in M1;									
CC	and (4) a method (M4) for identifying a candidate drug as a member of a									
CC	class of drugs having a characteristic effect on gene expression in a									
CC	yeast cell comprising contacting a yeast cell with a candidate drug and									
CC	monitoring expression in the yeast cell of at least 1 NORF gene whose									
CC	expression is affected by the class of drugs. The NORF genes may be used									
CC	to study, monitor and affect phases of the cell cycle, the differentially									
CC	expressed genes may be used as markers of phases of the cell cycle. The									
CC	methods may be used to identify candidate drugs which affect the cell									
CC	cycle and for identification of antifungal drugs. AAF33268 to AAF44064									
CC	represent SAGE tags used in the exemplification of the present invention.									
CC	AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE									
CC	method, in the exemplification of the present invention									
XX	XX									
XX	Sequence 10 BP; 6 A; 0 C; 2 G; 2 T; 0 U; 0 Other;									
XX	XX									
XX	Query Match	42.08;	Score 8.4;	DB 1;	Length 10;					
XX	Best Local Similarity	90.0%;	Pred. No. 83;							

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 623 AGAAGTCT 632
|||||
DB 10 AGAACTGCT 1

RESULT 146
AAF43948/c
ID AAF43948 standard; DNA; 10 BP.
XX AC AAF43948;
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:12087.
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UWJO) UNIV JOHNS HOPKINS.
XX PI Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 381; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention
XX Sequence 10 BP; 0 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
SQ

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 618 GGAAAGAAA 627
|||||
DB 10 GGGAAGAAA 1

RESULT 147
AAF34952
ID AAF34952 standard; DNA; 10 BP.
XX AC AAF34952;
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1691.
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UWJO) UNIV JOHNS HOPKINS.
XX PI Velulescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 60; 419pp; English.
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 617 CGAAAGAA 626
 Db 1 CAGAAAGAA 10
 RESULT 148
 AAF38358/c
 ID AAF38358 standard; DNA; 10 BP.
 XX
 AC AAF38358;
 DT 23-MAR-2001 (first entry)
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5097.
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velulescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 PS Example; Page 182; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 618 GGAAGAA 627
 Db 10 GGAATGAA 1
 RESULT 149
 AAF41701
 ID AAF41701 standard; DNA; 10 BP.
 XX
 AC AAF41701;
 DT 23-MAR-2001 (first entry)
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8440.
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velulescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 PS Example; Page 301; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 83;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 GAAAGTGCTG 633

Db 1 GAAAGAGCTG 10

RESULT 150

AAF35215

ID AAF35215 standard; DNA; 10 BP.

AC AAF35215;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1954.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

PN 21-DEC-2000.

PF 14-JUN-2000; 2000WO-US016223.

PR 16-JUN-1999; 99US-00335032.

PA (UYJO) UNIV JOHNS HOPKINS.

PI Velculescu V, Vogelstein B, Kinzler K;

DR WPI; 2001-061874/07.

PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

PS Example; Page 69; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX

SQ Sequence 10 BP; 6 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 83;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 AAAGAAAGT 629

Db 1 ACAAGAAAGT 10

RESULT 151

AAF36378/c

ID AAF36378 standard; DNA; 10 BP.

AC AAF36378;

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3117.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

PN 21-DEC-2000.

PF 14-JUN-2000; 2000WO-US016223.

PR 16-JUN-1999; 99US-00335032.

PA (UYJO) UNIV JOHNS HOPKINS.

PI Velculescu V, Vogelstein B, Kinzler K;

DR WPI; 2001-061874/07.

PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

PS Example; Page 111; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 GAAAGTCTG 633
DB 10 GAAAGTCTG 1
|||||
RESULT 152
ABSG4900/c
ID ABSG4900 standard; DNA; 10 BP.
XX
AC ABSG4900;
DT
DT 15-NOV-2002 (first entry)
XX
XX Primer-extension oligonucleotide, #3, for detecting CYP27B1 SNPs.
XX
XX Human; primer; ss; cytochrome P450; subfamily XXVIIIB;
KW 25-hydroxyvitamin D-1-alpha-hydroxylase; CYP27B1; isogene; hydroxylation;
KW 25-hydroxyvitamin D3; 25(OH)D3; calcitriol; 1alpha,25(OH)2D3; kidney;
KW nuclear receptor; vitamin D; VDR; calcium homeostasis;
KW cellular differentiation; SNP; single nucleotide polymorphism;
KW pseudovitamin D-dependent rickets type I; haplotyping; genotyping;
KW antibody; antisense; cancer; diabetes; inflammatory disorder;
KW chromosome 12q13.3-q14; antinflammatory;
KW primer-extension oligonucleotide.
XX
XX Homo sapiens.
XX
XX WO200262820-A2.
XX
XX 15-AUG-2002.
XX
XX 05-NOV-2001; 2001WO-US047438.
XX
XX 03-NOV-2000; 2000US-0245797P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Bieglecki KM, Monroe G, Kazemi A, Shah N;
XX
XX WPI; 2002-643397/69.
XX
XX
XX New genetic variants of the human polypeptide 1 (CYP27B1) gene, useful
PT for treating disorders associated with aberrant expression or
PT overproduction of TNF e.g. cancer, diabetes or inflammatory disorders.
XX
XX Claim 16; Page 15; 64pp; English.
PS
PS The invention discloses an isolated polymorphic polynucleotide comprising
CC a coding sequence for a cytochrome P450, subfamily XXVIIIB (25-
CC hydroxyvitamin D-1-alpha-hydroxylase) or CYP27B1 isogene. CYP27B1

CC catalyses the hydroxylation of 25-hydroxyvitamin D3 [25(OH)D3] to
CC calcitriol (1alpha,25(OH)2D3) in the proximal tubule of the kidney. The
CC binding of calcitriol to the nuclear receptor for the hormonally active
CC form of vitamin D (VDR) activates the receptor with subsequent regulation
CC of physiological events such as calcium homeostasis and cellular
CC differentiation. The various polymorphisms in the CYP27B1 gene may cause
CC pseudovitamin D-dependent rickets type I. The polynucleotide is useful
CC for haplotyping, genotyping, predicting a haplotype pair, identifying an
CC association between a trait and at least one haplotype or haplotype pair
CC and for designing an isolated nucleotide for detecting a polymorphism in
CC the CYP27B1 gene. The polypeptide is useful for raising antibodies
CC specific for, and immunoreactive with, the isolated polypeptide and for
CC screening for drugs or other chemical compounds that bind to, or are
CC enzymatic substrates for, the isolated polynucleotide. The pharmaceutical
CC composition, comprising the isolated polynucleotide, an antisense
CC oligonucleotide directed against one of the novel CYP27B1 isogenes, a
CC polynucleotide encoding the antisense oligonucleotide or another compound
CC that inhibits expression of the CYP27B1 isogene, is useful for treating
CC disorders affected by expression or function of the CYP27B1 isogene e.g.
CC cancer, diabetes or inflammatory disorders. The sequences presented in
CC ABS64898-ABS64911 are the primer-extension oligonucleotide primers which
CC were used for detecting CYP27B1 gene polymorphisms. The CYP27B1 gene is
CC located on chromosome 12q13.3-q14
XX
SQ Sequence 10 BP; 0 A; 3 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 621 AAGAGAAAGTG 630
DB 10 AAGAGAAAGCG 1
|||||
RESULT 153
ABLA42853
ID ABL42853 standard; cDNA; 10 BP.
XX
XX ABL42853;
XX
XX 12-APR-2002 (first entry)
XX
XX Human maturation/activation dendritic cell expression gene tag #227.
DE
XX Human; maturation/activation dendritic cell expression gene; tag;
KW maturation; activation; dendritic cell; ss.
XX
XX Homo sapiens.
XX
XX JP2001327293-A.
XX
XX 27-NOV-2001.
XX
XX 22-MAY-2000; 2000JP-00150562.
XX
XX 22-MAY-2000; 2000JP-00150562.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2002-127070/17.
XX
XX Human maturation/activation dendritic cell expression gene group.
XX
XX Claim 19; Page 15; 41pp; Japanese.
XX
XX The present invention describes a human maturation/activation dendritic
CC cell (DC) expression gene group consisting of 100 genes which show the
CC highest expression among the genes expressed in human maturation/
CC activation DC. Also described are: (1) a protein expressed by the above
CC human maturation/activation DC expression gene; (2) an antibody against
CC the protein; and (3) an antagonist against the expression of each gene
CC belonging to the above gene group. The gene group is useful for the

CC treatment and the diagnosis of various human diseases related to human
 CC DC. ABL42627 to ABL42926 represent specifically claimed human
 CC maturation/activation DC expression gene tags from the present invention
 XX SQ Sequence 10 BP; 7 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 620 AAAGAAAGT 629
 DB 1 AAAGAAAGT 10
 RESULT 154
 ABL42926/c
 ID ABL42926 standard; cDNA; 10 BP.
 XX AC ABL42926;
 XX DT 12-APR-2002 (first entry)
 XX DE Human maturation/activation dendritic cell expression gene tag #300.
 XX KW Human; maturation/activation dendritic cell expression gene; tag;
 KW maturation; activation; dendritic cell; ss.
 OS Homo sapiens.
 XX JN JP2001327293-A.
 PD 27-NOV-2001.
 XX PF 22-MAY-2000; 2000JP-00150562.
 XX PR 22-MAY-2000; 2000JP-00150562.
 XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX DR WPI; 2002-127070/17.
 XX PT Human maturation/activation dendritic cell expression gene group.
 XX PS Claim 19; Page 17; 41pp; Japanese.
 CC The present invention describes a human maturation/activation dendritic
 CC cell (DC) expression gene group consisting of 100 genes which show the
 CC highest expression among the genes expressed in human maturation/
 CC human maturation/activation DC expression gene; (2) an antibody against
 CC the protein; and (3) an antagonist against the expression of each gene
 CC belonging to the above gene group. The gene group is useful for the
 CC treatment and the diagnosis of various human diseases related to human
 CC DC. ABL42627 to ABL42926 represent specifically claimed human
 CC maturation/activation DC expression gene tags from the present invention
 XX SQ Sequence 10 BP; 2 A; 2 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 620 AAAGAAAGT 629
 DB 10 AAAGAAAGT 1
 RESULT 155
 ABK81442
 ID ABK81442 standard; DNA; 10 BP.
 XX AC ABK81442;
 CC treatment and the diagnosis of various human diseases related to human
 CC DC. ABL42627 to ABL42926 represent specifically claimed human
 CC maturation/activation DC expression gene tags from the present invention
 XX SQ Sequence 10 BP; 7 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 620 AAAGAAAGT 629
 DB 1 AAAGAAAGT 10
 RESULT 156
 ABQ72882/c
 ID ABQ72882 standard; DNA; 10 BP.
 XX AC ABQ72882;
 XX DT 06-SEP-2002 (first entry)
 XX DE Human GRM8 gene polymorphism detection primer, SEQ ID NO:86.
 XX KW Human; glutamate receptor metabotropic 8; GRM8; receptor;
 KW chromosome 7q31.3-32.1; neurotransmission; glutamate-mediated;
 KW Smith-Lemli-Opitz syndrome; retinitis pigmentosa;

XX 13-AUG-2002 (first entry)
 XX SCYA20 primer extension oligonucleotide #4.
 KW Small inducible cytokine subfamily A (Cys-Cys) member 20; SCYA20;
 KW polymorphism; haplotype; psoriasis; gene expression;
 KW primer extension oligonucleotide; ss.
 OS Homo sapiens.
 XX WO200232927-A2.
 XX PD 25-APR-2002.
 XX PF 19-OCT-2001; 2001WO-US046093.
 XX PR 19-OCT-2000; 2000US-0241725P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Bieglecki KM, Chew A, Russo DP, Sausker EA;
 XX WPI; 2002-435525/46.
 XX PT New genetic variants comprising haplotypes of the small inducible
 PT cytokine subfamily A, member 20 (SCYA20) gene, useful in improving the
 PT efficiency drug screening protocols for compounds (e.g. antipsoriatic
 PT drug) targeting SCYA20.
 XX PS Claim 16; Page 13; 62pp; English.
 XX The invention describes an isolated polynucleotide, which comprises genes
 CC and haplotypes of the small inducible cytokine subfamily A (Cys-Cys),
 CC member 20 (SCYA20) gene. The polynucleotide comprises polymorphic sites
 CC referred to as PS1-9 to designate the order in which they are located in
 CC the gene. The polymorphisms and haplotypes of SCYA20 gene are useful for
 CC validating whether SCYA20 is a suitable target for drugs to treat
 CC psoriasis and disorders associated with its abnormal expression or
 CC function, screening for such drugs and reducing bias in clinical trials
 CC of such drugs. Haplotype information would be useful in improving the
 CC efficiency and output of several steps in the drug discovery and
 CC development process, including target validation, identifying lead
 CC compounds, early phase clinical trials. The methods are useful in
 CC screening for compounds targeting SCYA20 to treat a specific condition or
 CC disease predicted to be associated with SCYA20 activity, e.g. psoriasis.
 CC This sequence represents a primer extension oligonucleotide used to
 CC identify polymorphisms in the SCYA20 gene
 XX SQ Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 616 CCGGAAAGA 625
 DB 1 CCGGAAAGA 10
 RESULT 156
 ABQ72882/c
 ID ABQ72882 standard; DNA; 10 BP.
 XX AC ABQ72882;
 XX DT 06-SEP-2002 (first entry)
 XX DE Human GRM8 gene polymorphism detection primer, SEQ ID NO:86.
 XX KW Human; glutamate receptor metabotropic 8; GRM8; receptor;
 KW chromosome 7q31.3-32.1; neurotransmission; glutamate-mediated;
 KW Smith-Lemli-Opitz syndrome; retinitis pigmentosa;

KW neuropathological disorder; neuroprotective; ophthalmological;
KW gene therapy; haplotyping; genotyping; haplotype; genetic variant;
KW single nucleotide polymorphism; SNP; drug screening; drug discovery;
KW primer extension; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200238587-A2.
XX
XX 16-MAY-2002.
XX
XX 09-NOV-2001; 2001WO-US047325.
XX
XX 09-NOV-2000; 2000US-0247576P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Bieglecki KM, Chew A, Choi JY, Koshy B, Parks KE;
XX
XX WPI; 2002-519291/55.
XX
XX Genetic variants of Glutamate Receptor, Metabotropic 8 isogenes, useful
XX for improving efficiency and reliability in drug development for treating
XX neuropathological conditions and retinitis pigmentosa.
XX
XX Claim 17; Page 15; 110pp; English.
XX
XX The invention relates to a method for haplotyping the glutamate receptor,
XX metabotropic 8 (GRM8) gene (ABQ72798, ABQ72905) of an individual, and
XX also describes 21 novel polymorphic sites within the human GRM8 gene. The
XX GRM8 gene is located on chromosome 7q31.3-32.1 and contains 10 exons
XX which encode a 908 amino acid protein (ABQ09564). GRM8 is involved in
XX glutamate-mediated neurotransmission, being a member of a subfamily of
XX metabotropic glutamate receptors that inhibit the activity of adenylate
XX cyclase in response to glutamate stimulation. The chromosomal location of
XX the GRM8 gene encompasses regions linked to Smith-Lemli-Opitz syndrome
XX and a form of retinitis pigmentosa. GRM8 nucleic acid sequences are
XX useful in studying the expression and function of GRM8, and in expressing
XX GRM8 protein for use in screening drugs for the treatment of GRM8-
XX associated diseases (e.g., neuropathological disorders, Smith-Lemli-Opitz
XX syndrome and retinitis pigmentosa). GRM8 nucleic acids and proteins are
XX also useful in studying the effect of polymorphisms on the biological
XX activity of GRM8. Polymorphisms in the target region may be determined by
XX the use of allele-specific oligonucleotides (ASOs; ABQ72800-ABQ72862) as
XX probes and primers, and by primer extension using oligonucleotide primers
XX comprising sequences ABQ72863-ABQ72904. The method of the invention is
XX useful for haplotyping the GRM8 gene in populations and in individuals,
XX enabling decisions to be made as to whether GRM8 is a likely therapeutic
XX target for a disease of interest, and in the design of clinical trials of
XX candidate drugs for treating GRM8-associated disorders. In addition,
XX transgenic animals comprising a human GRM8 gene are useful for studying
XX the expression of GRM8 isogenes in vivo, for in vivo screening and
XX testing of drugs targeted to GRM8, and for testing the efficacy of
XX therapeutic agents and compounds for treating GRM8-associated conditions
XX in a biological system. Sequences ABQ72863-ABQ72904 represent sequences
XX that are specifically claimed as components of primers used to detect
XX polymorphisms in the GRM8 gene by primer extension
XX
XX Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 624 GAAAGTCTCG 633
DB 10 GAAAGTCTCG 1

RESULT 157
ABL36382/c
ID ABL36382 standard; DNA; 10 BP.
XX

AC ABL36382;
XX
XX 22-APR-2002 (first entry)
XX
XX Human lysosomal acid phosphatase 2 primer-extension oligonucleotide 18.
XX
XX Human; ss; lysosomal acid phosphatase 2; ACP2; gene; chromosome 11;
XX lysosome-specific enzyme; orthophosphoric monoester hydrolysis;
XX Hodgkin's disease; HD; acid phosphatase deficiency;
XX novel polymorphic site; ACP2 haplotype; ACP2 genotype; polymorphism;
XX transgenic animal; primer; probe; primer-extension oligonucleotide; SNP;
XX single nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO200194362-A2.
XX
XX 13-DEC-2001.
XX
XX 07-JUN-2001; 2001WO-US018457.
XX
XX 07-JUN-2000; 2000US-0210047P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Kliem SE, Messer C, Tanguay DA;
XX
XX WPI; 2002-154563/20.
XX
XX Novel genetic variants of acid phosphatase 2, lysosomal polypeptide gene
XX useful in studying expression and function of the protein, and for
XX screening drugs to treat diseases e.g. Hodgkin's disease.
XX
XX Claim 19; Page 15; 109pp; English.
XX
XX The invention comprises the human lysosomal acid phosphatase 2 (ACP2)
XX nucleic acid and protein sequences. Specifically, the invention relates
XX to the discovery of 22 novel polymorphic sites within the ACP2 gene. The
XX invention also comprises methods for haplotyping and genotyping the ACP2
XX gene in an individual. The ACP2 gene (located on chromosome 11) encodes a
XX lysosomal-specific enzyme that catalyses the hydrolysis of
XX orthophosphoric monoesters to alcohol and phosphate. The ACP2 gene and
XX protein are pharmaceutically important in the treatment of Hodgkin's
XX disease (HD) and acid phosphatase deficiency. The novel ACP2 gene
XX polymorphisms of the invention are useful in haplotyping the ACP2 gene.
XX ACP2 haplotyping is useful in validating ACP2 as a target (and designing
XX drugs) for treating an ACP2-related disease or condition (e.g. Hodgkin's
XX disease and acid phosphatase deficiency). The ACP2 gene polymorphisms are
XX useful for ACP2 genotyping, which can also be used to develop diagnostic
XX tests and therapeutic treatments. The ACP2 protein and nucleic acids of
XX the invention are useful in the production of a transgenic animal which
XX expresses ACP2 protein. The ACP2 nucleic acids of the invention are
XX useful in the production of allele-specific oligonucleotides designed to
XX genotype each of the ACP2 polymorphisms. Nucleic acids ABL36299-ABL36320
XX represent claimed ACP2 allele-specific probes. Nucleic acids ABL36321-
XX ABL36384 represent claimed ACP2 allele-specific PCR primers. Nucleic
XX acids ABL36365-ABL36408 represent claimed ACP2 primer-extension
XX oligonucleotides
XX
XX Sequence 10 BP; 0 A; 3 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 618 GGAAGAGAAA 627
DB 10 GGAAGAGACA 1

RESULT 158
ADG28123
ID ADG28123 standard; DNA; 10 BP.

XX AC ADG28123;
 XX DT 26-FEB-2004 (first entry)
 XX DE Human Myo/VI protein-related NFKappaB regulation site SeqID127.
 XX KW cardiac-associated protein; Myo/VI protein; MP; cardiac; vasotropic;
 XX KW immunosuppressive; vulnary; NFKappaB p50; NFKappaB p65;
 XX KW cardiovascular disease; cardiac hypertrophy; myocardial infarction;
 XX KW ischaemia; reperfusion injury; heart transplantation;
 XX KW anti-ageing treatment; human; ds.
 XX OS Homo sapiens.
 XX PN WO200245659-A2.
 XX PD 13-JUN-2002.
 XX PF 26-OCT-2001; 2001WO-US051272.
 XX PR 27-OCT-2000; 2000US-0243985P.
 XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX PI Sivasubramanian N, Knuefermann P, Mann DL;
 XX DR WPI; 2002-537532/57.
 XX PT Novel dominant negative mutant sequence or constitutively active mutant
 PT sequence of Myo/VI polypeptide, useful for treating cardiovascular
 PT disorders and inhibiting formation of NFKappaB homodimers.
 XX PS Example 21; SEQ ID NO 127; 217pp; English.
 XX CC This invention relates to a novel dominant negative or constitutively
 CC active mutant sequence of the cardiac-associated Myo/VI protein (MP). The
 CC invention may be useful for the development of compounds with a cardiac,
 CC vasotropic, immunosuppressive or vulnary activity through the
 CC inhibition of formation of NFKappaB p50 or NFKappaB p65 homodimers. The
 CC invention may be useful for the development of treatments for
 CC cardiovascular disease including cardiac hypertrophy, myocardial
 CC infarction, ischaemia/reperfusion injury and heart transplantation, in a
 CC mammal, for anti-ageing treatment, for inhibiting formation of NFKappaB
 CC p50 homodimers or NFKappaB p65 homodimers in a cell of a mammal and for
 CC reducing formation of NFKappaB p65 homodimers in a cell of a mammal.
 XX Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 623 AGAAGTCT 632
 DB |||||
 1 AGAAGTCT 10
 RESULT 159
 ACA94429
 ID ACA94429 standard; DNA; 10 BP.
 XX AC ACA94429;
 XX DT 18-JUL-2003 (first entry)
 XX DE DNA tag from human transcript elevated in adenomas/cancers #10.
 XX KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
 KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
 KW kidney proximal tubule.
 XX OS Homo sapiens.

XX PN WO2003022863-A1.
 XX PD 20-MAR-2003.
 XX PF 09-SEP-2002; 2002WO-US028518.
 XX PR 07-SEP-2001; 2001US-0317494P.
 XX PR 30-MAY-2002; 2002US-0383805P.
 XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX PI Buckhaults P, Kinzler KW, Vogelstein B;
 XX DR WPI; 2003-313220/30.
 XX PT Detecting colorectal cancer in a subject, involves detecting macrophage
 PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
 PT of the subject.
 XX PS Disclosure; Page 25; 59pp; English.
 XX CC The invention relates to detecting CC (colorectal cancer e.g. colorectal
 CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
 CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
 CC amount of MIC or RDP detected to that in normal subjects, where an
 CC elevated amount of MIC or RDP in the subject is an indicator of CC in
 CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
 CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
 CC mRNA detected to that in normal subjects, where an elevated amount of MIC
 CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
 CC isolating epithelial cells from blood of a subject, isolating an mRNA
 CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
 CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
 CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
 CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
 CC of CC in the subject; (d) contacting blood or faeces of a subject, with
 CC an RDP substrate, detecting activity of RDP in the blood or faeces by
 CC detection of increased reaction product or decreased RDP substrate, and
 CC comparing the amount of activity of RDP in blood or faeces of the subject
 CC to that in normal subjects, where an elevated amount of activity of RDP
 CC in the blood or faeces of the subject is an indicator of CC in the
 CC subject; (e) administering to a subject an antibody which specifically
 CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
 CC labeled with a moiety which is detectable from outside of the subject and
 CC detecting the moiety in the subject from outside of the subject, where an
 CC area of localisation of the moiety within the subject but outside the
 CC proximal tubules of the kidney identifies CC; or (f) administering to a
 CC subject a substrate for RDP, the substrate being labeled with a
 CC detectable moiety, isolating faeces or blood from the subject, and
 CC detecting in the faeces or blood RDP reaction product or RDP substrate
 CC with the detectable moiety, where increased product or decreased
 CC substrate in the faeces or blood indicates CC in the subject. The methods
 CC are useful for detecting colorectal cancer in a subject. The present
 CC sequence is a DNA tag derived from a human transcript whose expression is
 CC elevated in colorectal cancer or colorectal adenoma
 XX Sequence 10 BP; 7 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 620 AAAAGAAAGT 629
 DB |||||
 1 AAAAGAAAGT 10
 RESULT 160
 ACC41709
 ID ACC41709 standard; DNA; 10 BP.
 XX AC ACC41709;
 AC

XX 21-MAY-2003 (first entry)
 DT Zinc finger protein DNA-binding domain target sequence SEQ ID NO:256.
 DE
 XX Zinc finger domain; zinc finger; zinc finger binding domain; probe;
 KW chimeric nucleic acid; library; PCR primer; ss.
 XX
 OS Synthetic.
 XX WO2003016571-A1.
 PN
 XX
 PD 27-FEB-2003.
 XX
 PF 17-AUG-2002; 2002WO-KR001560.
 XX
 XX 17-AUG-2001; 2001US-0313402P.
 PR
 XX 22-APR-2002; 2002US-0374355P.
 PR
 XX (TOOL-) TOOLGEN INC.
 PA
 XX Kim J, Bae K, Park K, Kwon Y, Ryu E, Hwang M;
 PI WPI; 2003-268344/26.
 XX
 XX New library comprising polypeptides having zinc finger domains, useful
 XX for producing chimeric nucleic acids.
 XX
 PS Claim 40; Page 105; 234pp; English.
 XX
 CC The present invention describes a library comprising polypeptides. Each
 CC polypeptide comprises a first or second zinc finger domain. The domains
 CC of each polypeptide are identical to a zinc finger domain from a
 CC naturally occurring protein and either do not occur in the same naturally
 CC occurring protein or occur in the same naturally occurring protein in a
 CC different configuration than in the polypeptide. The domains vary among
 CC polypeptides. Also described: (1) producing chimeric nucleic acids; (2)
 CC generating an artificial zinc finger polypeptide that specifically binds
 CC to a target DNA site; and (3) identifying a nucleic acid encoding a zinc
 CC finger polypeptide that specifically recognises a target DNA site. The
 CC library can be used for producing chimeric nucleic acids. ACC41551 to
 CC ACC41758 and ABR40919 to ABR41015 represent nucleotide and amino acid
 CC sequences given in the exemplification of the present invention
 XX
 XX Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. NO. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 617 CGGAAAGAA 626
 DB 1 CGGAAAGAA 10
 RESULT 161
 AAD60116
 ID AAD60116 standard; DNA; 10 BP.
 XX
 AC AAD60116;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human androgen-regulated gene (ARG) transcription regulator #5.
 XX
 KW Human; androgen-regulated gene; ARG; PNEPAL; prostate cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6566130-B1.
 XX
 XX 20-MAY-2003.
 PD

PF 26-JAN-2001; 2001US-00769482.
 XX
 PR 28-JAN-2000; 2000US-0178772P.
 PR 31-JAN-2000; 2000US-0179045P.
 XX
 PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 XX
 PT Srivastava S, Moul JW, Xu LL, Segawa T;
 PT WPI; 2003-719644/68.
 DR
 XX Novel isolated androgen-regulated gene designated as PNEPAL useful for
 XX selecting primers and probes for detecting prostate cancer cells in
 XX biological samples by nucleic acid amplification techniques.
 XX
 PS Example 7; Col 69; 58pp; English.
 XX
 CC The invention relates to an isolated androgen-regulated gene (ARG)
 CC designated as PNEPAL. The invention is useful for selecting primers and
 CC probes for detecting prostate cancer cells in a biological sample by
 CC using nucleic acid amplification techniques. The present sequence is
 CC human ARG transcription regulator oligonucleotide
 XX
 SQ Sequence 10 BP; 5 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. NO. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 619 GAAAGAAAG 628
 DB 1 GAAAGAAAG 10
 RESULT 162
 ADE14173
 ID ADE14173 standard; DNA; 10 BP.
 XX
 AC ADE14173;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Optineurin promoter motif, repeat element or regulatory region #282.
 XX
 KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
 KW SNP; glaucoma; progressive ocular hypertensive disorder;
 KW glaucoma related disorder; motif; repeat element; regulatory region.
 XX
 OS Homo sapiens.
 XX
 PN US2003190617-A1.
 XX
 PD 09-OCT-2003.
 XX
 PF 06-MAR-2002; 2002US-00091281.
 XX
 PR 06-MAR-2002; 2002US-00091281.
 XX
 PA (SIEE/) SI E.
 PA (RAYM/) RAYMOND V.
 PA (MORI/) MORISSETTE J.
 XX
 PI Raymond V, Morissette J, Si E;
 XX
 DR WPI; 2003-864168/80.
 XX
 PT New nucleic acid sequences of the optineurin gene are useful to detect
 PT polymorphisms particularly single nucleotide polymorphisms in the
 PT optineurin promoter to diagnose, prognose and treat glaucoma and related
 PT disorders.
 XX
 PS Claim 11; SEQ ID NO 284; 159pp; English.
 XX

CC The invention relates to an isolated nucleic acid (N1) comprising at
 CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
 CC promoter appearing as ADE13990. Also included are the optineurin promoter
 CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
 CC detecting a single nucleotide polymorphism (SNP) in the optineurin
 CC promoter, a host cell comprising the promoter operably linked to a
 CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 CC in a promoter region of the optineurin gene, associated with a glaucoma
 CC phenotype), detecting a SNP sequence variation in a sample containing
 CC DNA, detecting the presence of an optineurin promoter sequence variation
 CC in a sample containing DNA, determining the presence or increased
 CC susceptibility to glaucoma or to a progressive ocular hypertensive
 CC disorder resulting in loss of visual field in a patient for the severity
 CC or progression of glaucoma in a patient, comprising providing
 CC amplification reaction primers that direct amplification of a selected
 CC nucleic acid region containing the variation within the optineurin
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid
 CC capable of detecting a SNP located within an optineurin promoter, and
 CC detecting the polymorphism). The invention is used to diagnose and
 CC prognose glaucoma and also to treat glaucoma related disorders. The
 CC present sequence is an optineurin promoter motif, repeat element or
 CC putative regulatory region.

XX SQ Sequence 10 BP; 4 A; 1 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 623 AGAAGTGCT 632
 Db 1 AGAAGTGCT 10
 ||||| ||

RESULT 163
 ADG98629
 ID ADG98629 standard; DNA; 10 BP.
 AC ADG98629;
 XX 11-MAR-2004 (first entry)
 DE Human CETP gene allele specific extension PCR primer #90.
 KW human; cholesteryl ester transfer protein; CETP;
 KW single nucleotide polymorphism; SNP; drug screening; atherosclerosis;
 KW cardiovascular disease; hypercholesterolemia;
 KW allele specific oligonucleotide; ss; extension PCR; primer.

XX Homo sapiens.
 XX WO2003091277-A2.
 XX 06-NOV-2003.
 XX 28-APR-2003; 2003WO-US013288.
 XX 26-APR-2002; 2002US-037579P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Anastasio AE, Chew A, Kazemi A, Lachowicz M, Lee HH, Parks KE;
 PI Petersen N, Rounds E, Sauker EA, Tirrell C;
 XX WPI; 2003-865576/80.

XX New isolated polynucleotide useful for haplotyping and/or genotyping
 PT cholesteryl ester transfer protein (CETP) gene in an individual or in
 PT screening for drugs useful in treating diseases associated with CETP
 PT activity.

XX

PS Claim 45; SEQ ID NO 261; 250pp; English.
 XX The invention comprises the amino acid and coding sequences of the human
 CC cholesteryl ester transfer protein (CETP), the invention also comprises
 CC polymorphisms identified within the CETP gene. The DNA and protein
 CC sequences of the invention are useful in haplotyping and/or genotyping
 CC the CETP gene in an individual. The DNA and protein sequences may also be
 CC used to screen drugs or compounds targeting the CETP or its variant to
 CC treat a condition or disease associated with CETP (e.g. atherosclerosis,
 CC cardiovascular disease or hypercholesterolemia). The present DNA
 CC sequence represents an allele specific extension PCR primer for the human
 CC CETP gene.

XX SQ Sequence 10 BP; 6 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 42.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 83;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 618 GGAAGGAAA 627
 Db 1 GGAAGGAAA 10
 ||||| ||

RESULT 164
 ADG89969
 ID ADG89969 standard; DNA; 10 BP.
 AC ADG89969;
 XX 11-MAR-2004 (first entry)
 DE Human TNFRSF1A gene polymorphism detecting primer #5.
 KW Human; tumour necrosis factor receptor superfamily member 1A; TNFRSF1A;
 KW tumour; inflammatory disorder; immunological disorder; gene therapy;
 KW primer; polymorphism; ss.

XX Homo sapiens.
 XX US2003165844-A1.
 XX 04-SEP-2003.
 XX 31-AUG-2001; 2001US-00945505.
 XX 31-AUG-2001; 2001US-00945505.
 XX (GENA-) GENAISSANCE PHARM INC.

XX Anastasio AE, Chew A, Denton RR, Nandabalan K, Parks KE;
 PI Stephens JC;
 XX WPI; 2003-898046/82.
 XX Haplotyping tumor necrosis factor receptor superfamily member 1A
 PT (TNFRSF1A) gene of an individual comprises identifying the phased
 PT sequence of nucleotides at each polymorphic site on a copy of the
 PT individual's TNFRSF1A gene.

XX Claim 17; SEQ ID NO 29; 65pp; English.
 XX The present invention provides novel genetic variants of human tumour
 CC necrosis factor receptor superfamily, member 1A (TNFRSF1A) gene. The
 CC invention also relates to compositions and methods for haplotyping and/or
 CC genotyping TNFRSF1A gene in an individual. Methods and compositions of
 CC the invention are used to screen drugs targeting the TNFRSF1A protein to
 CC treat a condition or disease predicted to be associated with TNFRSF1A
 CC activity. The disease or condition include tumours, inflammatory
 CC disorders or immunological disorders. The invention is also useful in
 CC gene therapy. The present sequence is a primer used to detect human
 CC TNFRSF1A gene polymorphisms.

XX

SQ Sequence 10 BP; 6 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 619 GAAAGAAAG 628
| | | | |
Db 1 GTAAGAAAG 10
RESULT 165
ADH62225
ID ADHG2225 standard; DNA; 10 BP.
XX
AC ADH62225;
DT 25-MAR-2004 (first entry)
XX
DE Human transcription regulator #5.
XX
KW Androgen-regulated gene; ARG; PMPAL; therapy; diagnosis; prognosis;
KW prostate cancer; hormonal therapy; human; ds.
XX Homo sapiens.
OS
XX US2003170713-Al.
PN
PD 11-SEP-2003.
XX
PF 18-MAR-2003; 2003US-00390045.
XX
PR 28-JAN-2000; 2000US-0178772P.
PR 31-JAN-2000; 2000US-0179045P.
PR 26-JAN-2001; 2001US-00769482.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
XX Srivastava S, Moul JW, Xu LL, Segawa T;
FI WPI; 2003-898255/82.
XX
XX Polynucleotide array, useful for diagnosing or prognosing prostate
PT cancer, comprises a planar, non-porous solid support and a set of
PT polynucleotide probes attached to the solid support.
XX
PS Example 7; SEQ ID NO 17; 61pp; English.
XX
XX The present invention relates to the identification and characterisation
CC of a novel androgen-regulated genes (ARGs) that exhibits abundant
CC expression in prostate tissue. The novel gene is designated PMPAL. The
CC invention is useful for diagnosing and prognosing prostate cancer. The
CC invention is also useful in hormonal therapy. The present sequence is
CC androgen-regulated gene fragment.
XX
SQ Sequence 10 BP; 6 A; 0 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 619 GAAAGAAAG 628
| | | | |
Db 1 GAAAGAAAG 10
RESULT 166
ADH75077
ID ADH75077 standard; DNA; 10 BP.
XX
AC ADH75077;
XX
DT 22-APR-2004 (first entry)

XX
DE Photodamage detection method related DNA #95.
XX
KW personal care method; photodamage; Serial Analysis of Gene Expression;
KW SAGE; sun-damage; pre-auricular skin; sun-protected post-auricular;
KW sun-protected epidermis; aging; dry skin; oily skin; photodamage marker;
KW ss.
XX
OS Homo sapiens.
XX
PN US2003152964-Al.
XX
PD 14-AUG-2003.
XX
PF 07-OCT-2002; 2002US-00266138.
XX
PR 08-NOV-2001; 2001US-0338272P.
XX
PA (UNIL) UNILEVER HOME & PERSONAL CARE USA DIV CO.
XX
PI Iobst ST, Schilling KM, Boyd C, Urschitz J;
XX
XX WPI; 2003-635999/60.
DR
XX Personal care method for detecting photodamage, aging, dry or oily skin
PT comprises detecting gene markers upregulated in pre-auricular skin.
PT
XX
PS Example 2; Page 10; 25pp; English.
XX
XX The invention describes a personal care method of detecting photodamage
CC comprising comparative Serial Analysis of Gene Expression (SAGE) of sun-
CC damaged pre-auricular skin and sun-protected post-auricular skin as well
CC as sun-protected epidermis. The method involves: using at least one
CC marker of photodamage comprising one of 15 fully defined sequences (S1-
CC 15) as given in the specification; and detecting a change in the marker
CC to determine the presence of photodamage. The method is useful for
CC detecting photodamage, aging, dry skin or oily skin. This sequence
CC represents a SAGE sequence tag used as a marker for detecting photodamage
CC in skin.
XX
SQ Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 619 GAAAGAAAG 628
| | | | |
Db 1 GAAAGAAAG 10
RESULT 167
ADH75117
ID ADH75117 standard; DNA; 10 BP.
XX
AC ADH75117;
XX
DT 22-APR-2004 (first entry)
XX
DE Photodamage detection method related DNA #135.
XX
KW personal care method; photodamage; Serial Analysis of Gene Expression;
KW SAGE; sun-damage; pre-auricular skin; sun-protected post-auricular;
KW sun-protected epidermis; aging; dry skin; oily skin; photodamage marker;
KW ss.
XX
OS Homo sapiens.
XX
PN US2003152964-Al.
XX
PD 14-AUG-2003.
XX
PF 07-OCT-2002; 2002US-00266138.

XX PR 08-NOV-2001; 2001US-0338272P.
XX PA (UNIL) UNILEVER HOME & PERSONAL CARE USA DIV CO.
XX PI Iobst ST, Schilling KM, Boyd C, Urschitz J;
XX DR WPI; 2003-635999/60.
XX PT Personal care method for detecting photodamage, aging, dry or oily skin
XX PT comprises detecting gene markers upregulated in pre-auricular skin.
XX PS Example 2; Page 12; 25pp; English.
XX CC The invention describes a personal care method of detecting photodamage
XX CC comprising comparative Serial Analysis of Gene Expression (SAGE) of sun-
XX CC damaged pre-auricular skin and sun-protected post-auricular skin as well
XX CC as sun-protected epidermis. The method involves: using at least one
XX CC marker of photodamage comprising one of 15 fully defined sequences (S1-
XX CC 15) as given in the specification; and detecting a change in the marker
XX CC to determine the presence of photodamage. The method is useful for
XX CC detecting photodamage, aging, dry skin or oily skin. This sequence
XX CC represents a SAGE sequence tag used as a marker for detecting photodamage
XX CC in skin.
XX SQ Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 619 GAAAGAAAG 628
Db ||||| |||||
1 GAAAGAAAG 10
RESULT 168
ADH75057
ID ADH75057 standard; DNA; 10 BP.
XX AC ADH75057;
XX DT 22-APR-2004 (first entry)
XX DE Photodamage detection method related DNA #75.
XX KW personal care method; photodamage; Serial Analysis of Gene Expression;
XX KW SAGE; sun-damage; pre-auricular skin; sun-protected post-auricular;
XX KW sun-protected epidermis; aging; dry skin; oily skin; photodamage marker;
XX KW ss.
XX OS Homo sapiens.
XX PN US2003152964-A1.
XX PD 14-AUG-2003.
XX PF 07-OCT-2002; 2002US-00266138.
XX PR 08-NOV-2001; 2001US-0338272P.
XX PA (UNIL) UNILEVER HOME & PERSONAL CARE USA DIV CO.
XX PI Iobst ST, Schilling KM, Boyd C, Urschitz J;
XX DR WPI; 2003-635999/60.
XX PT Personal care method for detecting photodamage, aging, dry or oily skin
XX PT comprises detecting gene markers upregulated in pre-auricular skin.
XX PS Example 2; Page 9; 25pp; English.
XX CC The invention describes a personal care method of detecting photodamage

XX CC comprising comparative Serial Analysis of Gene Expression (SAGE) of sun-
XX CC damaged pre-auricular skin and sun-protected post-auricular skin as well
XX CC as sun-protected epidermis. The method involves: using at least one
XX CC marker of photodamage comprising one of 15 fully defined sequences (S1-
XX CC 15) as given in the specification; and detecting a change in the marker
XX CC to determine the presence of photodamage. The method is useful for
XX CC detecting photodamage, aging, dry skin or oily skin. This sequence
XX CC represents a SAGE sequence tag used as a marker for detecting photodamage
XX CC in skin.
XX SQ Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 619 GAAAGAAAG 628
Db ||||| |||||
1 GAAAGAAAG 10
RESULT 169
ADM77072
ID ADM77072 standard; cDNA; 10 BP.
XX AC ADM77072;
XX DT 03-JUN-2004 (first entry)
XX DE Photodamage marker #79.
XX KW ss; photodamage; skin; aging; drying; human.
XX KW ss.
XX OS Homo sapiens.
XX PN US2003170739-A1.
XX PD 11-SEP-2003.
XX PF 07-OCT-2002; 2002US-00265509.
XX PR 08-NOV-2001; 2001US-0337856P.
XX PA (UNIL) UNILEVER HOME & PERSONAL CARE USA DIV CO.
XX PI Iobst ST, Schilling KM, Boyd C, Urschitz J;
XX DR WPI; 2003-830613/77.
XX PT Detection of skin conditions e.g. photodamage, aging and drying,
XX PT comprises using polynucleotide sequences in gene arrays as markers, and
XX PT detecting a change in the markers.
XX PS Example 2; Page 9; 21pp; English.
XX CC The invention relates a method to the detection of photodamage comprising
XX CC using a marker of photodamage and detecting a change in the marker to
XX CC determine the presence of photodamage. The marker is a nucleic acid
XX CC having cDNA sequence of 11 or 10 base pairs. Detection is done by
XX CC comparing a first skin sample with a second skin sample to determine a
XX CC change in a marker. The method is used for detecting a skin condition,
XX CC e.g. photodamage, aging and drying. The method provides an easy way to
XX CC track expression of even small numbers of genes in laboratory models or
XX CC in human tissue. The present sequence represents a photodamage marker
XX CC used in the method of the invention.
XX SQ Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 619 GAAAGAAAG 628

DR WPI; 2004-081932/08.
XX Protein in the nuclei of human and animal cells associated with
PT expression of retinoblastoma-1 gene for diagnosis of cancer.
XX
PS Disclosure; Page 11; 113pp; Japanese.
XX
CC The invention relates to a protein or polypeptide found in the nuclei of
CC human and animal cells that are associated with transcription and/or
CC induction of expression of retinoblastoma-1 gene (RB1CC1). The detection
CC of RB1CC1 gene and its protein is useful for the diagnosis of cancer. The
CC human RB1CC1 cDNA is 6.6 kb containing a 4782 bp ORF, encoding a 180 kD
CC 1594 amino acid protein. This sequence corresponds to the sequence at the
CC junction between an intron and an exon in the human RB1CC1 genomic
CC sequence.
XX
SQ Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 616 CCGGAAAGCA 625
DB 10 CTGGAAAGCA 1
RESULT 173
ADM33248
ID ADM33248 standard; DNA; 10 BP.
XX
AC ADM33248;
XX
DT 17-JUN-2004 (first entry)
XX
DE Oligo SEQ ID 83, used in method for estimating melting temperature.
XX
KW Melting temperature; probe design; primer design; ss.
XX
OS Synthetic.
XX
FN WO2004025257-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028664.
XX
PR 12-SEP-2002; 2002US-0410663P.
XX
PA (INTE-) INTEGRATED DNA TECHNOLOGIES INC.
XX
PI Owczarzy R, Walder JA, Huang L, Behlke MA;
XX
DR WPI; 2004-340203/31.
XX
PT Estimating melting temperature, for designing or selecting
PT oligonucleotide probes or primers, comprises modifying the reference
PT melting temperature by a logarithm of the ratio of the desired ion to the
PT reference ion concentrations.
XX
PS Example 1; Page 41; 66pp; English.
XX
CC The present invention relates to a method for estimating a melting
CC temperature (Tm) for a polynucleotide at a desired ion concentration
CC having a known G-C content value. The method is useful for designing and
CC selecting oligonucleotide probes and primers. The present sequence was
CC used to illustrate the method of the invention.
XX
SQ Sequence 10 BP; 6 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
DB 1 GAAATGAAAG 10

RESULT 174

ADO39842
ID ADO39842 standard; DNA; 10 BP.

XX
AC ADO39842;
XX
DT 29-JUL-2004 (first entry)
XX
DE Androgen-regulated gene (ARG) fragment #5.
XX
KW Androgen-regulated gene; ARG; PMEPAL; prostate cancer; Cap;
KW prostate-related disease; gene therapy; vaccine; ds.
XX
OS Unidentified.
XX
FN US2004092469-A1.
XX
PD 13-MAY-2004.
XX
PF 09-MAY-2003; 2003US-00434479.
XX
PR 28-JAN-2000; 2000US-0178772P.
PR 31-JAN-2000; 2000US-0179045P.
PR 26-JAN-2001; 2001US-00769482.
PR 18-MAR-2003; 2003US-00390045.
XX
PA (SRIV/) SRIVASTAVA S.
PA (MOUL/) MOUL J W.
PA (XULL/) XU L L.
XX
PI Srivastava S, Moul JW, Xu LL;
XX
DR WPI; 2004-374986/35.

XX
PT New PMEPAL polypeptide that inhibits the growth of LN prostate cancer
PT (LNCap) cells in a colony-forming assay, useful for detecting, preventing
PT and treating prostate cancer.

XX
PS Example 6; SEQ ID NO 17; 78pp; English.

XX
CC The invention relates to androgen-regulated gene (ARG), PMEPAL and its
CC encoded protein. PMEPAL polypeptide is useful in inhibiting the growth of
CC a prostate cancer (Cap) cell. It is also useful for reducing the
CC expression of an androgen receptor or modulating the expression of a gene
CC in a prostate cancer cell. PMEPAL sequence is useful in gene therapy,
CC useful to prepare vaccines, useful as markers of prostate cancer and
CC other prostate-related diseases, and as targets for therapeutic
CC intervention in prostate cancer and other prostate-related diseases.
CC PMEPAL, its encoding nucleic acid or the antibodies are useful for
CC detecting, preventing and treating prostate cancer. The present sequence
CC is an androgen-regulated gene fragment which has transcription regulating
CC activity.

XX
SQ Sequence 10 BP; 6 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 GAAAGAAAG 628
DB 1 GAAAGAAAG 10

RESULT 175

AAQ96028/c

ID AAQ96028 standard; DNA; 8 BP.

XX AC AAQ96028;
 XX DT 09-SEP-2004 (revised)
 XX DT 19-MAR-1996 (first entry)
 XX DE Oligonucleotide #17 for discrimination of mismatched hybrids.
 XX KW Oligomer; non-specific; complementary; target sequence; hypoxanthine;
 KW inosine; pairing; base pair; solid support; aminolink; diagnosis;
 KW infectious; hereditary disease; genome mapping; sensitivity; mismatch;
 KW hybridisation; D value; ss.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT misc_difference 1 /*tag= a
 FT /note= "linked to solid support via an aminolink 2"
 XX EP668361-A1.
 XX PD 23-AUG-1995.
 XX PF 21-FEB-1995; 95EP-00102435.
 XX PR 22-FEB-1994; 94JP-00024168.
 XX PR 29-JUN-1994; 94JP-00147291.
 XX PA (MITU) MITSUBISHI CHEM CORP.
 XX PI Fuguno N, Kurusu Y, Terasawa M, Yukawa H;
 XX WPI; 1995-284795/38.
 XX DR An oligo:nucleotide with a degenerate non-standard base hybridises with -
 PT a target sequence in a sample oligo:nucleotide, for improved
 PT discrimination of mismatched hybrids.
 XX PS Example B; Page 8; 23pp; English.
 XX CC The oligonucleotides AAQ96015-42 are oligomers contg. a specific region
 CC which is complementary to the target sequence and a non-specific region
 CC at one or both ends of the specific region. The non-specific region is
 CC composed of bases having a non-standard base e.g. hypoxanthine, which is
 CC capable of loose pairing with standard nucleotides. The oligomers are
 CC pref. attached to a solid support by an aminolink 2 at the 5' end. The
 CC oligomers AAQ96028-42 are targeted to the target DNA sample AAQ96027. The
 CC oligonucleotides are useful for the diagnosis of infectious or hereditary
 CC diseases and in genome mapping. The oligonucleotides increase the
 CC sensitivity of hybridisation because the presence of completely
 CC complementary hybrids can be distinguished from mismatched hybrids (D
 CC value as high as 24 can be achieved)
 CC Revised record issued on 09-SEP-2004 : Correction to feature table key
 XX SQ Sequence 8 BP; 0 A; 3 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 618 GGAAAGA 625
 DB 8 GGAAAGA 1
 RESULT 176
 ADF67928
 ID ADF67928 standard; DNA; 9 BP.
 XX AC ADF67928;
 XX

DT 12-FEB-2004 (first entry)
 XX Human APC gene, -related sequence #1.
 XX KW Human; APC; adenomatous polyposis coli; digital protein truncation test;
 KW Dig-PT; ss; colorectal cancer; cytostatic; VHL; von Hippel-landau; CP;
 KW cystic fibrosis; hMSH2; hMLH1; hPMS2;
 KW hereditary non-polyposis colorectal cancer.
 XX OS Homo sapiens.
 XX PN US2003165940-A1.
 XX PD 04-SEP-2003.
 XX PF 02-DEC-2002; 2002US-00307505.
 XX PR 06-DEC-2001; 2001US-0336177P.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Traverso CG, Kinzler KW, Vogelstein B;
 XX WPI; 2004-059248/06.
 XX DR Detecting tumors by protein truncation assay using a body sample that has
 PT been divided up to contain few allele templates per reaction increases
 PT sensitivity to allow early stage detection and in samples with a high
 PT number of other alleles.
 XX PS Disclosure; SEQ ID NO 5; 21pp; English.
 XX CC The invention relates to detecting tumours comprising dividing a test
 CC sample of alleles into a number of aliquots, amplifying the alleles,
 CC transcribing and translating proteins in vitro using the amplified
 CC alleles as templates, and determining size or composition of the
 CC proteins, where a difference from the protein produced by the wild-type
 CC allele indicates a mutation in the amplified allele and thus a tumour in
 CC the patient, the method is known as digital protein truncation test (Dig-
 CC PT). The gene is preferably adenomatous polyposis coli (APC), and at
 CC least a portion of exon 15 including codons 1210 through 1581 of APC is
 CC amplified. The allele may be isolated from a stool sample. Alternatively
 CC the gene is VHL and the disease is von Hippel-landau, the gene is CF and
 CC the disease is cystic fibrosis, or the gene is hMSH2, hMLH1 or hPMS2 and
 CC the disease is hereditary non-polyposis colorectal cancer. The invention
 CC is useful to detect cancer particularly colorectal cancer, especially
 CC adenomatous polyposis coli, von Hippel-landau or hereditary non-polyposis
 CC colorectal cancer, in the early stages and in samples, particularly stool
 CC samples, containing high levels of other alleles. The assay is more
 CC sensitive than prior art, allowing detection of a mutated allele among
 CC many wild type alleles. APC mutations can be identified through in vitro
 CC transcription and translation reactions as most mutations result in a
 CC premature stop codon producing truncated proteins. The present sequence
 CC is a sequence included in the sequence listing but not mentioned anywhere
 CC else in the patent.
 XX SQ Sequence 9 BP; 7 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 621 AAAGAAAG 628
 DB 1 AAAGAAAG 8
 RESULT 177
 ADR01088
 ID ADR01088 standard; DNA; 9 BP.
 XX AC ADR01088;
 XX

PD 12-JAN-1995.
XX
XX 28-JUN-1994; 94WO-US007319.
XX
XX 02-JUL-1993; 93US-00088658.
PR
PA (ISIS-) ISIS PHARM INC.
XX
XX Buchardt O, Egholm M, Nielsen PE, Berg RH, Ecker DJ;
PI Mollegaard NE;
PI
XX
XX WPI; 1995-060949/08.
DR
XX Use of oligonucleotide analogues, partic. peptide nucleic acids - for
PT binding to ssDNA, dsDNA or RNA for use in therapy, diagnosis and
PT prophylaxis.
PT
XX
XX Disclosure; Page 25; 139pp; English.
PS
XX
XX AAQ81104 is a peptide nucleic acid (PNA), which binds a target sequence.
CC The binding of the PNA prevents the transcription of the target sequence.
CC by RNA polymerase. The ability of the PNA to arrest transcription makes
CC it useful in gene therapy, and in diagnostic and prophylactic methods.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC
XX Sequence 10 BP; 0 A; 1 C; 0 G; 9 T; 0 U; 0 Other;
SQ

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
DB 10 AAAAGAAA 3

RESULT 180.
AAQ81102
ID AAQ81102 standard; DNA; 10 BP.
XX
XX AC AAQ81102;
XX
XX 25-MAR-2003 (revised)
DT 28-SEP-1995 (first entry)
XX
XX Peptide nucleic acid target sequence.
DE
XX Peptide nucleic acid; gene therapy; transcription arrest;
KW target sequence; diagnosis; prophylaxis; ds.
KW
XX Synthetic.
OS
XX WO9501370-AL.
PN
XX 12-JAN-1995.
XX
XX 28-JUN-1994; 94WO-US007319.
PF
XX 02-JUL-1993; 93US-00088658.
PR
XX (ISIS-) ISIS PHARM INC.
XX
XX Buchardt O, Egholm M, Nielsen PE, Berg RH, Ecker DJ;
PI Mollegaard NE;
PI
XX
XX WPI; 1995-060949/08.
DR
XX Use of oligonucleotide analogues, partic. peptide nucleic acids - for
PT binding to ssDNA, dsDNA or RNA for use in therapy, diagnosis and
PT prophylaxis.
PT
XX
XX Disclosure; Page 25; 139pp; English.
PS
XX

CC AAQ81099 and AAQ81100 are peptide nucleic acids (PNAs), which bind the
CC target sequences described in AAQ81101-Q81104. The binding of the PNAs
CC prevents the transcription of the target sequences by the RNA polymerases
CC T3 and T7. The ability of the PNAs to arrest transcription makes them
CC useful in gene therapy, and in diagnostic and prophylactic methods.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 10 BP; 9 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
SQ

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
DB 2 AAAAGAAA 9

RESULT 181
AAQ81121/c
ID AAQ81121 standard; DNA; 10 BP.
XX
XX AC AAQ81121;
XX
XX 25-MAR-2003 (revised)
DT 28-SEP-1995 (first entry)
XX
XX Peptide nucleic acid.
DE
XX Peptide nucleic acid; gene therapy; transcription arrest; diagnosis;
KW prophylaxis; ss.
KW
XX Synthetic.
OS
XX Key Location/Qualifiers
FT misc_feature 4..5
FT /*tag= a
FT /note= "Beta-alanine in sequence"
FT modified_base 10
FT /*tag= b
FT /note= "covalently bound Lys-NH2 group"
XX
XX WO9501370-AL.
PN
XX 12-JAN-1995.
XX
XX 28-JUN-1994; 94WO-US007319.
PF
XX 02-JUL-1993; 93US-00088658.
PR
XX (ISIS-) ISIS PHARM INC.
XX
XX Buchardt O, Egholm M, Nielsen PE, Berg RH, Ecker DJ;
PI Mollegaard NE;
PI
XX
XX WPI; 1995-060949/08.
DR
XX Use of oligonucleotide analogues, partic. peptide nucleic acids - for
PT binding to ssDNA, dsDNA or RNA for use in therapy, diagnosis and
PT prophylaxis.
PT
XX
XX Example 1; Page 28; 139pp; English.
PS
XX AAQ81121 is a peptide nucleic acid (PNA), which binds a target sequence.
CC The binding of the PNA prevents the transcription of the target sequence.
CC by RNA polymerase. The ability of the PNA to arrest transcription makes
CC it useful in gene therapy, and in diagnostic and prophylactic methods.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC
XX Sequence 10 BP; 0 A; 1 C; 0 G; 9 T; 0 U; 0 Other;
SQ

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;

```

Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      620 AAAAGAAA 627
Db      |||||
        9 AAAAGAAA 2

RESULT 182
AAQ96677
ID AAQ96677 standard; DNA; 10 BP.
XX AC AAQ96677;
XX
XX 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 272.
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX
XX 17-AUG-1995.
PD
XX 14-FEB-1995; 95WO-AU000063.
PF
XX
XX 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 272.
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX
XX 17-AUG-1995.
PD
XX 14-FEB-1995; 95WO-AU000063.
PF
XX
XX 14-FEB-1994; 94AU-00003864.
PR
XX 21-FEB-1994; 94AU-00004002.
PR
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 191; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 8 A; 0 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      620 AAAAGAAA 627
Db      |||||
        2 AAAAGAAA 9

RESULT 183
AAQ96678
ID AAQ96678 standard; DNA; 10 BP.
XX AC AAQ96678;
XX
XX 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 271.
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX
XX 17-AUG-1995.
PD
XX 14-FEB-1995; 95WO-AU000063.
PF
XX
XX 14-FEB-1994; 94AU-00003864.
PR
XX 21-FEB-1994; 94AU-00004002.
PR
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 191; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 8 A; 0 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

XX HIV-1 NL4-3 nef gene nucleotide deletion 273.
DE
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX Human immunodeficiency virus 1.
OS
XX WO9521912-A1.
PN
XX 17-AUG-1995.
PD
XX 14-FEB-1995; 95WO-AU000063.
PF
XX
XX 14-FEB-1994; 94AU-00003864.
PR
XX 21-FEB-1994; 94AU-00004002.
PR
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 191; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 8 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      620 AAAAGAAA 627
Db      |||||
        1 AAAAGAAA 8

RESULT 184
AAQ96676
ID AAQ96676 standard; DNA; 10 BP.
XX AC AAQ96676;
XX
XX 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 271.
DE
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX
XX 17-AUG-1995.
PD
XX 14-FEB-1995; 95WO-AU000063.
PF
XX
XX 14-FEB-1994; 94AU-00003864.
PR
XX 21-FEB-1994; 94AU-00004002.
PR
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 191; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 8 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

PR 23-DEC-1994; 94AU-00000284.
 XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
 PA (AURE-) AUSTRALIAN RED CROSS SOC.
 PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
 XX WPI; 1995-293115/38.
 DR
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
 PT LTR region - can be used in a vaccine to inhibit/reduce productive
 PT infection in an individual by a pathogenic strain.
 XX
 PS Claim 13; Page 191; 301pp; English.
 XX
 CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
 CC resulting avirulent HIV strains are still capable of inducing an immune
 CC response in humans, and enable the generation of therapeutic, diagnostic
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 10 BP; 7 A; 0 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 620 AAAAGAAA 627
 DB 3 AAAAGAAA 10
 |||||
 RESULT 185
 AAV50338
 ID AAV50338 standard; DNA; 10 BP.
 XX
 AC AAV50338;
 XX
 XX 21-OCT-1998 (first entry)
 DT
 DE Yeast tag for additional NORF chromosome 15 tag position 882567.
 XX
 KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
 KW eukaryotic cell; antifungal; SAGE tag; gene expression;
 KW serial analysis of gene expression; probe; ss.
 XX
 OS Saccharomyces cerevisiae.
 OS Synthetic.
 XX
 XX WO9832847-A2.
 FN
 XX 30-JUL-1998.
 PD
 XX
 XX 22-JAN-1998; 98WO-US001216.
 PF
 XX
 XX 23-JAN-1997; 97US-0035917P.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PA
 XX Velulescu VE, Vogelstein B, Kinzler KW;
 PI WPI; 1998-427943/36.
 DR
 XX Yeast transcriptome - useful for modulating eukaryotic cell, for
 PT screening antifungal agents, and for identifying genes in cell cycle
 PT progression.
 PT
 XX Claim 1; Page 27; 44pp; English.
 PS
 XX Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene

CC involved in cell cycle progression selected from the group of
 CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
 CC tags for highly expressed genes and NORF genes are given in AAV50051 to
 CC AAV50345. The present invention describes: (1) a method of using yeast
 CC genes to modulate the cell cycle which comprises administering to a cell
 CC an isolated DNA molecule comprising a yeast gene which is involved in
 CC cell cycle progression selected from differentially expressed genes (SAGE
 CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate
 CC antifungal drugs which comprises contacting a test substance with a yeast
 CC cell and monitoring expression of a yeast gene which is involved in cell
 CC cycle progression; (3) a method of identifying human genes which are
 CC involved in cell cycle progression which comprises hybridizing a probe
 CC comprising at least 10 contiguous nucleotides of a yeast gene which is
 CC differentially expressed between at least 2 phases selected from the log
 CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
 CC the phase in the cell cycle, where the probe comprises at least 14
 CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
 CC AAV50345), or as an array of probes on a solid support
 XX
 SQ Sequence 10 BP; 9 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 620 AAAAGAAA 627
 DB 3 AAAAGAAA 10
 |||||
 RESULT 186
 AAV11235
 ID AAV11235 standard; DNA; 10 BP.
 XX
 AC AAV11235;
 XX
 XX 17-OCT-2003 (revised)
 DT
 DT 15-JUL-1998 (first entry)
 XX
 DE Seq ID #51 from WO9803542.
 XX
 KW Peptide nucleic acid; PNA; aminoethyl-glycine backbone; effector ligand;
 KW aminoethyl-lysine; 1-8C alkylamine side chain; gene modulation;
 KW diagnostic; triple helix; treatment; infection; genetic disorder; ss.
 XX
 OS unidentified.
 XX
 XX WO9803542-A1.
 PN
 XX 29-JAN-1998.
 PD
 XX 24-JUL-1997; 97WO-US012811.
 PF
 XX 24-JUL-1996; 96US-00685484.
 PR
 XX 24-JUL-1996; 96US-00686113.
 PR
 XX 24-JUL-1996; 96US-00686114.
 PR
 XX 24-JUL-1996; 96US-00886116.
 PR
 XX 29-MAY-1997; 97US-0051002P.
 PR
 XX (BUCH/) BUCHARDT D.
 PA (ISIS-) ISIS PHARM INC.
 PA
 XX Nielsen P, Egholm M, Berg RH, Buchardt O;
 PI WPI; 1998-145251/13.
 DR
 XX New peptide nucleic acid compound(s) containing 1-8Calkyl:amine side
 PT chains - have improved solubility and show enhanced sequence specificity
 PT and binding affinity for complementary DNA or RNA.
 PT
 XX Disclosure; Page 128; 150pp; English.
 PS
 XX This invention describes peptide nucleic acids (PNAs) which exhibit

CC enhanced solubility, sequence specificity and binding affinity for
 CC complementary DNA or RNA, due to incorporation of the 1-8C alkylamine
 CC side chain. The PNAs described above may be linked to low molecular
 CC weight effector ligands (e.g. reporter ligands such as fluorescent
 CC ligands), peptides/proteins with signalling activity (e.g. enzymes,
 CC transcription factors or antibodies), water-(in)soluble polymers,
 CC oligonucleotides or carbohydrates. The PNAs may be used in gene
 CC modulation, diagnostic purposes, biotechnology or other research
 CC purposes. They may be modified in such a way that they form triple
 CC helices with double stranded DNA (and may thus be used in treatment of
 CC cancer, AIDS, other viral infections or genetic disorders). Note:
 CC Sequences AAV11225-V11237 are not described within the specification but
 CC are given in the sequence listing. (Updated on 17-OCT-2003 to standardise
 CC OS field)
 CC
 CC Sequence 10 BP; 9 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
 Db 1 AAAAGAAA 8
 |||||

RESULT 187
 ID AAV11233 standard; DNA; 10 BP.
 XX AC AAV11233;
 XX
 DT 17-OCT-2003 (revised)
 DT 15-JUL-1998 (first entry)
 DE Seq ID #49 from WO9803542.
 XX
 XX Peptide nucleic acid; PNA; aminoethyl-glycine backbone; effector ligand;
 KW aminoethyl-lysine; 1-8C alkylamine side chain; gene modulation;
 KW diagnostic; triple helix; treatment; infection; genetic disorder; ss.
 XX
 OS unidentified.
 XX
 XX WO9803542-A1.
 XX
 XX 29-JAN-1998.
 XX
 XX 24-JUL-1997; 97WO-US012811.
 XX
 XX 24-JUL-1996; 96US-00685484.
 XX 24-JUL-1996; 96US-00686113.
 XX 24-JUL-1996; 96US-00686114.
 XX 24-JUL-1996; 96US-00686116.
 XX 29-MAY-1997; 97US-0051002P.
 XX
 XX (BUCH/) BUCHARDT D.
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Nielsen P, -Egholm M, Berg RH, Buchardt O;
 XX WPI; 1998-145251/13.
 DR
 XX New peptide nucleic acid compound(s) containing 1-8Calkyl:amine side
 PT chains - have improved solubility and show enhanced sequence specificity
 PT and binding affinity for complementary DNA or RNA.
 XX
 XX Disclosure; Page 127; 150pp; English.
 PS
 XX This invention describes peptide nucleic acids (PNAs) which exhibit
 CC enhanced solubility, sequence specificity and binding affinity for
 CC complementary DNA or RNA, due to incorporation of the 1-8C alkylamine
 CC side chain. The PNAs described above may be linked to low molecular
 CC weight effector ligands (e.g. reporter ligands such as fluorescent

CC ligands), peptides/proteins with signalling activity (e.g. enzymes,
 CC transcription factors or antibodies), water-(in)soluble polymers,
 CC oligonucleotides or carbohydrates. The PNAs may be used in gene
 CC modulation, diagnostic purposes, biotechnology or other research
 CC purposes. They may be modified in such a way that they form triple
 CC helices with double stranded DNA (and may thus be used in treatment of
 CC cancer, AIDS, other viral infections or genetic disorders). Note:
 CC Sequences AAV11225-V11237 are not described within the specification but
 CC are given in the sequence listing. (Updated on 17-OCT-2003 to standardise
 CC OS field)
 CC
 CC Sequence 10 BP; 9 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
 Db 2 AAAAGAAA 9
 |||||

RESULT 188
 ID AAZ78164 standard; DNA; 10 BP.
 XX AC AAZ78164;
 XX
 DT 10-APR-2000 (first entry)
 DE Human dendritic cell SAGE tag, SEQ ID NO:592.
 XX
 XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9965924-A2.
 XX
 XX 23-DEC-1999.
 PD
 XX 18-JUN-1999; 99WO-US013800.
 XX
 XX 19-JUN-1998; 98US-0089833P.
 XX 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089991P.
 PR 19-JUN-1998; 98US-0089992P.
 PR 19-JUN-1998; 98US-0089993P.
 PR 19-JUN-1998; 98US-0089994P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090035P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.

PR 08-DEC-1998; 98US-0111715P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX WPI; 2000-106077/09.
 DR
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 XX
 XX Claim 1; Page 82; 130pp; English.
 XX
 XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 6 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 618 GGAAGAAGA 625
 Db |||||
 2 GGAAGAAGA 9
 RESULT 189
 AAZ78206
 ID AAZ78206 standard; DNA; 10 BP.
 XX
 XX AAZ78206;
 AC
 AC 10-APR-2000 (first entry)
 DT
 XX Human dendritic cell SAGE tag, SEQ ID NO:634.
 DE
 XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX Homo sapiens.
 OS
 PN WO9965924-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013800.
 XX
 PR 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089991P.
 PR 19-JUN-1998; 98US-0089992P.
 PR 19-JUN-1998; 98US-0089993P.
 PR 19-JUN-1998; 98US-0089994P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090035P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX WPI; 2000-106077/09.
 DR
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 XX
 XX Claim 1; Page 83; 130pp; English.
 XX
 XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal

expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

XX Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 623 AGAAGTG 630
|||||||
Db 1 AGAAGTG 8

RESULT 190
AAZ85759/c
ID AAZ85759 standard; DNA; 10 BP.
XX
AC AAZ85759;
DT 07-APR-2000 (first entry)
DE Metastatic breast tumour cell downregulated transcript tag #4993.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
XX
PS Claim 1; Page 191; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 CC to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These CC transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is

by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in CC vaccines; for diagnosing breast cancer and for raising specific CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic CC agents. Host cells that produce the polypeptides can be used to expand CC and isolate populations of educated, antigen-specific immune effector CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive CC immunotherapy

XX
SQ Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 AAAGAAAG 628
|||||||
Db 10 AAAGAAAG 3

RESULT 191
AAZ85029
ID AAZ85029 standard; DNA; 10 BP.
XX
AC AAZ85029;
DT 07-APR-2000 (first entry)
DE Metastatic breast tumour cell downregulated transcript tag #4263.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
XX
PS Claim 1; Page 172; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 CC to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These CC transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is

transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy

Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 628 GTGCTGGA 635
Db 1 GTGCTGGA 8
|||||||

RESULT 192
AAZ82002
ID AAZ82002 standard; DNA; 10 BP.
XX AAZ82002;
XX
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1236.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX OS
XX WO9965928-A2.
XX PN
XX 23-DEC-1999.
XX PD
XX 18-JUN-1999; 99WO-US013647.
XX PF
XX 19-JUN-1998; 98US-0089853P.
XX PR
XX 19-JUN-1998; 98US-0089997P.
XX PR
XX 19-JUN-1998; 98US-0090039P.
XX PR
XX 19-JUN-1998; 98US-0090040P.
XX PR
XX 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX PI
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
XX PT
XX
XX Claim 1; Page 91; 219pp; English.
XX PS
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are

preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy

Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 628 GTGCTGGA 635
Db 2 GTGCTGGA 9
|||||||

RESULT 193
AAZ84727/C
ID AAZ84727 standard; DNA; 10 BP.
XX AAZ84727;
XX
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3961.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX OS
XX WO9965928-A2.
XX PN
XX 23-DEC-1999.
XX PD
XX 18-JUN-1999; 99WO-US013647.
XX PF
XX 19-JUN-1998; 98US-0089853P.
XX PR
XX 19-JUN-1998; 98US-0089997P.
XX PR
XX 19-JUN-1998; 98US-0090039P.
XX PR
XX 19-JUN-1998; 98US-0090040P.
XX PR
XX 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX PI
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
XX PT
XX
XX Claim 1; Page 164; 219pp; English.
XX PS
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour

transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy

Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 628 GTGCTGGA 635
Db 2 GTGCTGGA 9
|||||||

RESULT 193
AAZ84727/C
ID AAZ84727 standard; DNA; 10 BP.
XX AAZ84727;
XX
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3961.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX OS
XX WO9965928-A2.
XX PN
XX 23-DEC-1999.
XX PD
XX 18-JUN-1999; 99WO-US013647.
XX PF
XX 19-JUN-1998; 98US-0089853P.
XX PR
XX 19-JUN-1998; 98US-0089997P.
XX PR
XX 19-JUN-1998; 98US-0090039P.
XX PR
XX 19-JUN-1998; 98US-0090040P.
XX PR
XX 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX PI
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
XX PT
XX
XX Claim 1; Page 164; 219pp; English.
XX PS
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour

X

XX

PS Claim 1; Page 166; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts

CC that are preferentially transcribed in the metastatic breast tumour

CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942

CC to AAZ86677 represent tags corresponding to distinct transcripts that are

CC preferentially transcribed in the primary or non-metastatic breast tumour

CC tissue (i.e. are downregulated in metastatic breast tumour cells). These

CC transcripts can be used for diagnosis, prognosis, monitoring and

CC treatment of breast cancer, particularly where metastatic. Diagnosis is

CC by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially

CC useful for treatment of (metastatic) breast cancer, while promoters from

CC the transcripts are used to direct expression, in selected cell types, of

CC e.g. therapeutic genes (also ribozymes or antisense sequences),

CC particularly an antigen-encoding sequence for use in gene or cell-based

CC vaccines. Polypeptides encoded by the transcripts are also useful in

CC vaccines; for diagnosing breast cancer and for raising specific

CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic

CC agents. Host cells that produce the polypeptides can be used to expand

CC and isolate populations of educated, antigen-specific immune effector

CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive

CC immunotherapy

XX Sequence 10 BP; 0 A; 1 C; 1 G; 8 T; 0 U; 0 Other;

SQ Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAA 627

DB 8 AAAAGAA 1

RESULT 196

AAZ84861/c

ID AAZ84861 standard; DNA; 10 BP.

XX AAZ84861;

AC AAZ84861;

DT 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #4095.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;

XX non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WO9965928-A2.

PN 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-008997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

PI WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

PT non-metastatic breast cancer cells, useful for diagnosis, prevention and

PS Claim 1; Page 167; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts

CC that are preferentially transcribed in the metastatic breast tumour

CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942

CC to AAZ86677 represent tags corresponding to distinct transcripts that are

CC preferentially transcribed in the primary or non-metastatic breast tumour

CC tissue (i.e. are downregulated in metastatic breast tumour cells). These

CC transcripts can be used for diagnosis, prognosis, monitoring and

CC treatment of breast cancer, particularly where metastatic. Diagnosis is

CC by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially

CC useful for treatment of (metastatic) breast cancer, while promoters from

CC the transcripts are used to direct expression, in selected cell types, of

CC e.g. therapeutic genes (also ribozymes or antisense sequences),

CC particularly an antigen-encoding sequence for use in gene or cell-based

CC vaccines. Polypeptides encoded by the transcripts are also useful in

CC vaccines; for diagnosing breast cancer and for raising specific

CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic

CC agents. Host cells that produce the polypeptides can be used to expand

CC and isolate populations of educated, antigen-specific immune effector

CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive

CC immunotherapy

XX Sequence 10 BP; 1 A; 2 C; 0 G; 7 T; 0 U; 0 Other;

SQ Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAA 626

DB 8 GAAAGAA 1

RESULT 197

AAZ83013

ID AAZ83013 standard; DNA; 10 BP.

XX AAZ83013;

AC AAZ83013;

DT 07-APR-2000 (first entry)

XX Metastatic breast tumour cell upregulated transcript tag #2247.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;

XX non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WO9965928-A2.

PN 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-008997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

PI WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

PT non-metastatic breast cancer cells, useful for diagnosis, prevention and

Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.

Claim 1; Page 119; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy.

Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 AAAGAAG 628
DB 1 AAAGAAG 8

RESULT 198

AAZ81715/c

ID AAZ81715 standard; DNA; 10 BP.

AC AAZ81715;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #949.

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO9965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US013647.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-008997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PA (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

DR

XX WPI; 2000-106079/09.

PT Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.

PS Claim 1; Page 84; 219pp; English.

AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effector cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy.

Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 GAAAGAA 626

DB 10 GAAAGAA 3

RESULT 199

AAZ85291

ID AAZ85291 standard; DNA; 10 BP.

AC AAZ85291;

DT 07-APR-2000 (first entry)

DE Metastatic breast tumour cell downregulated transcript tag #4525.

KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

PN WO9965928-A2.

PD 23-DEC-1999.

PF 18-JUN-1999; 99WO-US013647.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-008997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

PA (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX

PI Roberts BL, Shankara S;
 XX WPI; 2000-106079/09.
 DR
 XX
 PT Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 180; 219pp; English.
 CC
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 XX Sequence 10 BP; 6 A; 0 C; 3 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 618 GGAARAAGA 625
 DB 2 GGAARAAGA 9
 RESULT 200
 AAH63545
 ID AAH63545 standard; cDNA; 10 BP.
 XX
 AC AAH63545;
 XX
 DT 20-SEP-2001 (first entry)
 DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 385.
 XX
 XX Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200138577-A2.
 PN
 PD 31-MAY-2001.
 XX
 XX 21-NOV-2000; 2000WO-US031922.
 PF
 XX 24-NOV-1999; 99US-00448480.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velulescu VE, Vogelstein B, Kinzler KW;
 PI WPI; 2001-367706/38.
 DR
 XX
 XX New isolated polynucleotides, useful for identifying specific cell type,
 PT cancer diagnosis; cell specific gene expression; ss.
 PT
 PT Homo sapiens.
 XX
 PS WO200138577-A2.
 XX
 XX 31-MAY-2001.
 PD
 XX 21-NOV-2000; 2000WO-US031922.
 PF
 XX 24-NOV-1999; 99US-00448480.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velulescu VE, Vogelstein B, Kinzler KW;
 PI WPI; 2001-367706/38.
 DR
 XX New isolated polynucleotides, useful for identifying specific cell type,
 PT cancer diagnosis; cell specific gene expression; ss.
 PT

PT such as cancer cell, comprises transcriptomes expressed in particular
 PT cell types.
 XX
 PS Claim 13; Page 47; 94pp; English.
 XX
 CC The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH63161-
 CC AAH64724 is expressed by the cell. The transcriptomes described in the
 CC invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcriptomes described in the exemplification of the invention
 XX
 SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 628 GTGCTGGA 635
 DB 2 GTGCTGGA 9
 RESULT 201
 AAH63707
 ID AAH63707 standard; cDNA; 10 BP.
 XX
 AC AAH63707;
 XX
 DT 20-SEP-2001 (first entry)
 DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 547.
 XX
 XX Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200138577-A2.
 PN
 PD 31-MAY-2001.
 XX
 XX 21-NOV-2000; 2000WO-US031922.
 PF
 XX 24-NOV-1999; 99US-00448480.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velulescu VE, Vogelstein B, Kinzler KW;
 PI WPI; 2001-367706/38.
 DR
 XX
 XX New isolated polynucleotides, useful for identifying specific cell type,
 PT cancer diagnosis; cell specific gene expression; ss.
 PT
 PT Homo sapiens.
 XX
 PS Claim 13; Page 51; 94pp; English.
 XX
 CC The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH63161-
 CC AAH64724 is expressed by the cell. The transcriptomes described in the
 CC invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcriptomes described in the exemplification of the invention
 XX
 SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 628 GTGCTGGA 635
 DB 2 GTGCTGGA 9
 RESULT 201
 AAH63707
 ID AAH63707 standard; cDNA; 10 BP.
 XX
 AC AAH63707;
 XX
 DT 20-SEP-2001 (first entry)
 DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 547.
 XX
 XX Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200138577-A2.
 PN
 PD 31-MAY-2001.
 XX
 XX 21-NOV-2000; 2000WO-US031922.
 PF
 XX 24-NOV-1999; 99US-00448480.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velulescu VE, Vogelstein B, Kinzler KW;
 PI WPI; 2001-367706/38.
 DR
 XX
 XX New isolated polynucleotides, useful for identifying specific cell type,
 PT cancer diagnosis; cell specific gene expression; ss.
 PT
 PT Homo sapiens.
 XX
 PS Claim 13; Page 51; 94pp; English.
 XX
 CC The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH63161-
 CC AAH64724 is expressed by the cell. The transcriptomes described in the
 CC invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcriptomes described in the exemplification of the invention
 XX
 SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 628 GTGCTGGA 635
 DB 2 GTGCTGGA 9
 RESULT 201
 AAH63707
 ID AAH63707 standard; cDNA; 10 BP.
 XX
 AC AAH63707;
 XX
 DT 20-SEP-2001 (first entry)
 DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 547.
 XX
 XX Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200138577-A2.
 PN
 PD 31-MAY-2001.
 XX
 XX 21-NOV-2000; 2000WO-US031922.
 PF
 XX 24-NOV-1999; 99US-00448480.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velulescu VE, Vogelstein B, Kinzler KW;
 PI WPI; 2001-367706/38.
 DR
 XX
 XX New isolated polynucleotides, useful for identifying specific cell type,
 PT cancer diagnosis; cell specific gene expression; ss.
 PT

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 628 GTGCTGGA 635
 |||||
 1 GTGCTGGA 8

Db

RESULT 202
 AAH64124
 ID AAH64124 standard; cDNA; 10 BP.

XX
 AC AAH64124;
 XX
 DT 20-SEP-2001 (first entry)
 XX
 DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 964.
 XX
 KW Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200138577-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 21-NOV-2000; 2000WO-US031922.
 XX
 PR 24-NOV-1999; 99US-00448480.
 XX
 PA (UJJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu VE, Vogelstein B, Kinzler KW;
 DR WPI; 2001-367706/38.
 XX
 PT New isolated polynucleotides, useful for identifying specific cell type,
 PT such as cancer cell, comprises transcriptomes expressed in particular
 PT cell types.
 XX
 PS Claim 13; Page 61; 94pp; English.
 XX
 CC The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH63161-
 CC AAH64724 is expressed by the cell. The transcriptomes described in the
 CC invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcriptomes described in the exemplification of the invention
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 628 GTGCTGGA 635
 |||||
 1 GTGCTGGA 8

Db

RESULT 203
 AAF81044/c
 ID AAF81044 standard; DNA; 10 BP.

XX
 AC AAF81044;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE Primer for detecting PTGS polymorphisms by primer extension SEQ ID 150.
 DE Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;
 KW

KW single nucleotide polymorphism; SNP; immune-related disorder; arthritis;
 KW inflammation; primer; ss.
 OS Homo sapiens.
 XX
 PN WO200107662-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-US020114.
 XX
 PR 22-JUL-1999; 99US-0145170P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;
 DR WPI; 2001-182805/18.
 XX
 PT New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,
 PT for gene therapy of inflammation and for establishing a genotype or
 PT haplotype.
 XX
 PS Disclosure; Page 24; 118pp; English.
 XX
 CC This invention relates to a polynucleotide sequence that is a polymorphic
 CC variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene
 CC also referred to as cyclooxygenase 2. The human PTGS2 gene sequence
 CC AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and
 CC AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2
 CC protein is represented by AAB72199. The invention includes PCR and
 CC sequencing primers, and probes represented in AAF80898 - AAF81151 which
 CC are used to isolate and characterise the PTGS2 gene sequence, and to
 CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide
 CC sequences are used to express variant PTGS2 proteins, for structural
 CC analysis or drug-binding studies and also in gene therapy (either
 CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are
 CC useful for diagnosis, prognosis and therapy and analysis of the new, and
 CC known, polymorphisms and used to determine PTGS2 haplotype and genotype,
 CC especially for determining association between a particular trait, e.g. a
 CC clinical response to drugs that target PTGS2 but also disease
 CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly
 CC used for developing diagnostic tests and treatments for immune-related
 CC disorders such as arthritis and inflammation. The polymorphisms may also
 CC be used to study expression and biological function of PTGS2. Transgenic
 CC animals that express PTGS2 are used to study expression of PTGS2
 CC isogenes, for in vivo drug screening and testing, and for assessing
 CC effects of therapeutic agents
 XX
 SQ Sequence 10 BP; 0 A; 1 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
 |||||
 10 AAAAGAAA 3

Db

RESULT 204
 AAF36878
 ID AAF36878 standard; DNA; 10 BP.

XX
 AC AAF36878;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3617.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 OS WO200077214-A2.
 XX 21-DEC-2000.
 PD 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 PF (UYJO) UNIV JOHNS HOPKINS.
 XX Velculescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Example; Page 129; 419pp; English.
 PS The present invention describes an isolated DNA molecule comprising a
 XX coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX Sequence 10 BP; 9 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 620 AAAAGAAA 627
 Db 3 AAAAGAAA 10
 RESULT 205
 AAF39485/C
 ID AAF39485 standard; DNA; 10 BP.
 XX AC AAF39485;
 XX 23-MAR-2001 (first entry)
 DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6224.
 XX

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 OS WO200077214-A2.
 XX 21-DEC-2000.
 PD 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 PF (UYJO) UNIV JOHNS HOPKINS.
 XX Velculescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX Example; Page 222; 419pp; English.
 PS The present invention describes an isolated DNA molecule comprising a
 XX coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;
 SQ Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 622 AAGAAAGT 629
 Db 8 AAGAAAGT 1
 RESULT 206
 AAF36657/C
 ID AAF36657 standard; DNA; 10 BP.
 XX AC AAF36657;
 XX 23-MAR-2001 (first entry)
 DT

```

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3396.
DE
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS WO200077214-A2.
XX
XX
XX WO200077214-A2.
XX
XX
XX 21-DEC-2000.
XX
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 121; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF4064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 0 A; 2 C; 1 G; 7 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 621 AAAGAAAG 628
DB 10 AAAGAAAG 3
RESULT 207
AAF37047
ID AAF37047 standard; DNA; 10 BP.
XX

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AC AAF37047;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3786.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS WO200077214-A2.
XX
XX
XX 21-DEC-2000.
XX
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
XX gene expression (SAGE) tags, useful for studying, monitoring and
XX affecting phases of the cell cycle.
XX
XX Example; Page 135; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
XX coding sequence of a yeast gene selected from a group of 745 NORF (not
XX previously assigned open reading frame; or nonannotated ORF) genes
XX comprising a SAGE (serial analysis of gene expression) tag. Also
XX described are: (1) a method (M1) of using NORF genes to affect the cell
XX cycle comprising administering a NORF gene whose expression varies by at
XX least 10% between any two phases of the cell cycle selected from log
XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX antifungal drugs comprising: (a) contacting a test substance with a yeast
XX cell; and (b) monitoring expression of a NORF gene whose expression of
XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX identifying human genes which are involved in cell cycle progression
XX comprising contacting human DNA with a probe which comprises at least 10
XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX and (4) a method (M4) for identifying a candidate drug as a member of a
XX class of drugs having a characteristic effect on gene expression in a
XX yeast cell comprising contacting a yeast cell with a candidate drug and
XX monitoring expression in the yeast cell of at least 1 NORF gene whose
XX expression is affected by the class of drugs. The NORF genes may be used
XX to study, monitor and affect phases of the cell cycle, the differentially
XX expressed genes may be used as markers of phases of the cell cycle. The
XX methods may be used to identify candidate drugs which affect the cell
XX cycle and for identification of antifungal drugs. AAF33268 to AAF4064
XX represent SAGE tags used in the exemplification of the present invention.
XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
SQ
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 621 AAAGAAAG 628
DB 3 AAAGAAAG 10
RESULT 208

```

AAAF36327/c
ID AA36327 standard; DNA; 10 BP.
XX
AC AA36327;
DT
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3066.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 109; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 619 GAAAGAA 626
DB 9 GAAAGAA 2

RESULT 209
AAAF36916
ID AA36916 standard; DNA; 10 BP.
XX
AC AA36916;
DT
DT 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3655.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 130; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
XX Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 625 AAAGTGCT 632
 DB 1 AAAGTGCT 8

RESULT 210
 ID AAF42384/C
 AC AAF42384 standard; DNA; 10 BP.
 XX
 AC AAF42384;
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9123.
 XX
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 XX 14-JUN-2000; 2000WO-US016223.
 PF
 XX 16-JUN-1999; 99US-00335032.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velculescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 325; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF3262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 627 AGTGCTGG 634
 DB 9 AGTGCTGG 2

RESULT 211
 ID AAF42677
 AC AAF42677;
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:10816.
 XX
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 XX 14-JUN-2000; 2000WO-US016223.
 PF
 XX 16-JUN-1999; 99US-00335032.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velculescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 336; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF3262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX

SQ Sequence 10 BP; 5 A; 1 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 622 AAGAAAGT 629
|||||||
DB 3 AAGAAAGT 10

RESULT 212
AAF41024/C
ID AAF41024 standard; DNA; 10 BP.
XX
AC AAF41024;
DT
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7763.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX WO200077214-A2.
XX PN
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PP
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
DR Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 277; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle. The
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 628 GTGCTGGA 635
|||||||
DB 10 GTGCTGGA 3

RESULT 213
AAF33555
ID AAF33555 standard; DNA; 10 BP.
XX
AC AAF33555;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:294.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX WO200077214-A2.
XX PN
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PP
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
DR Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Claim 1; Page 27; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle. The
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.

CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF3262 to AAF3267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 9 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 620 AAAGAAA 627
 Db 3 AAAGAAA 10
 RESULT 214
 AAF39862
 ID AAF39862 standard; DNA; 10 BP.
 AC AAF39862;
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6601.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velulescu V, Vogelstein B, Kinzler K;
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 PS Example; Page 235; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF3268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF3262 to AAF3267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 7 A; 0 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 621 AAAGAAA 628
 Db 3 AAAGAAA 10
 RESULT 215
 AAF36127
 ID AAF36127 standard; DNA; 10 BP.
 XX
 AC AAF36127;
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2866.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velulescu V, Vogelstein B, Kinzler K;
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 PS Example; Page 102; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a

varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF4064 represent SAGE tags used in the exemplification of the present invention. CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

XX Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 628 GTGCTGGA 635
|||||||
Db 9 GTGCTGGA 2

RESULT 218
AAF34701/C
ID AAF34701 standard; DNA; 10 BP.
AC AAF34701;
DT 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1440.
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
OS WO200077214-A2.
PN 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
PF 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
PA Velculescu V, Vogelstein B, Kinzler K;
PI WPI; 2001-061874/07.
DR Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 51; 419pp; English.
PS The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF4064 represent SAGE tags used in the exemplification of the present invention. CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

XX Sequence 10 BP; 0 A; 1 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
|||||||
Db 9 AAAAGAAA 2

RESULT 219
AAF38720
ID AAF38720 standard; DNA; 10 BP.
XX AAF38720;
AC AAF38720;
DT 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5459.
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
OS WO200077214-A2.
PN 21-DEC-2000.
XX 14-JUN-2000; 2000WO-US016223.
PF 16-JUN-1999; 99US-00335032.
XX (UYJO) UNIV JOHNS HOPKINS.
PA Velculescu V, Vogelstein B, Kinzler K;
PI WPI; 2001-061874/07.
DR Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 195; 419pp; English.
PS The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log

described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 616 CCGGAAAA 623
DB 3 CCGGAAAA 10
|||||

RESULT 220
AAF34650/c
ID AAF34650 standard; DNA; 10 BP.
XX AAF34650;
DT 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1389.
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
OS
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
DR Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX Example; Page 49; 419pp; English.
PS
CC The present invention describes an isolated DNA molecule comprising a

coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.

Sequence 10 BP; 0 A; 1 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAAAGAAA 627
DB 10 AAAAGAAA 3
|||||

RESULT 221
AAF35643/c
ID AAF35643 standard; DNA; 10 BP.
XX AAF35643;
AC AAF35643;
XX
DT 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2382.
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX Saccharomyces cerevisiae.
OS
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
DR Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX

PS Example; Page 85; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 0 A; 1 C; 1 G; 8 T; 0 U; 0 Other;

SQ Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 620 AAAAGAAA 627

DB 10 AAAAGAAA 3

RESULT 222

AAF38421

ID AAF38421 standard; DNA; 10 BP.

XX AAF38421;

AC AAF38421;

XX 23-MAR-2001 (first entry)

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5160.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

PN WO200077214-A2.

XX 21-DEC-2000.

PD 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

PR (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX Example; Page 184; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 9 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

SQ Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 620 AAAAGAAA 627

DB 2 AAAAGAAA 9

RESULT 223

AAF43757

ID AAF43757 standard; DNA; 10 BP.

XX AAF43757;

AC AAF43757;

XX 23-MAR-2001 (first entry)

DT 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11896.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

PN WO200077214-A2.

XX 21-DEC-2000.

PD 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

PR (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

PI

DR WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX Example; Page 374; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 5 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

SQ Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 GGAAAGA 625

Db 3 GGAAAGA 10

RESULT 224

ABK86470

XX ID ABK86470 standard; cDNA; 10 BP.

XX AC ABK86470;

XX 27-AUG-2002 (first entry)

XX Human apo-dystrophin-4 direct repeat region sequence #1.

XX Human; ss; apo-dystrophin-4; inversion sequence; gene therapy;

XX protein truncation; muscular dystrophy; leukaemia.

XX Homo sapiens.

XX Key Location/Qualifiers

FT repeat_region 1..8

FT /*tag= a

FT /rpt_type= DIRECT

FT repeat_unit 1..4

FT /*tag= b

FT misc_recomb 10

FT /*tag= c

FT /label= Inversion_breakpoint

XX GB2368064-A.

XX 24-APR-2002.

XX 16-JAN-2001; 2001GB-00001124.

XX 30-SEP-2000; 2000US-0237079P.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX (BARB/) BARBER E.

XX Barber E;

XX WPI; 2002-429042/46.

XX New human regulatory polynucleotide, useful for treating disorders

PT associated with protein truncation, particularly muscular dystrophy, and

PT related peptides and antibodies.

XX Disclosure; Fig 16B; 222pp; English.

XX The invention relates to a polynucleotide (I) comprising, or consisting

CC of, apo-dystrophin-4 inversion sequence appearing as ABK86496, or its

CC functional equivalents (e.g. the apo-dystrophin-4 cDNA sequence appearing

CC as ABK86497). Also included are polynucleotides that hybridise to either

CC strand of (I), a vector containing (I), a cell containing (I) or the

CC vector, proteins and peptides encoded by (I), a protein homologous with

CC human dystrophin that is expressed on cell surfaces in vivo antibodies

CC (Ab) specific for the protein and method of screening for leukemia cells

CC by analysing DNA for presence of (I) or by detecting presence of (II).

CC The apo-dystrophin-4 inversion sequence is a regulatory element that

CC controls expression (transcription and translation) of associated DNA,

CC and may allow read-through of stop codons. The apo-dystrophin-4 inversion

CC sequence is used in gene therapy of diseases associated with truncation

CC of proteins, particularly muscular dystrophy and also leukaemia, but more

CC generally (I) is a regulatory sequence used to control expression of any

CC attached gene. Analysis of DNA for (I), or detection of proteins (II)

CC encoded by (I), can be used to screen for leukemic cells and related

CC diseases. Antibodies raised against (II) can be used therapeutically, to

CC inhibit (II) activity, also to detect (II) in screening assays. The

CC present sequence is a apo-dystrophin-4 cDNA fragment showing the first

CC direct repeat thought to be responsible for the inversion present in apo-

CC dystrophin-4

XX Sequence 10 BP; 7 A; 0 C; 2 G; 1 T; 0 U; 0 Other;

SQ Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 621 AAAGAAAG 628

Db 1 AAAGAAAG 8

RESULT 225

ABK86076/c

XX ID ABK86076 standard; cDNA; 10 BP.

XX AC ABK86076;

XX 27-AUG-2002 (first entry)

XX Human apo-dystrophin-4 direct repeat region sequence #2.

XX Human; ss; apo-dystrophin-4; inversion sequence; gene therapy;

XX protein truncation; muscular dystrophy; leukaemia.

XX Homo sapiens.

XX Key Location/Qualifiers

FT misc_recomb 1

FT /*tag= a

FT /label= Inversion_breakpoint

XX FT

FT repeat_region 3..10 /tag= b
 FT /rpt_type= DIRECT
 FT repeat_unit 3..6
 FT /tag= c
 XX
 PN CB2368064-A.
 XX
 PD 24-APR-2002.
 XX
 PF 16-JAN-2001; 2001GB-00001124.
 XX
 PR 30-SEP-2000; 2000US-0237079P.
 XX
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 PA (BARB/) BARBER E.
 XX
 PI Barber E;
 XX
 DR WPI; 2002-429042/46.
 XX
 PT New human regulatory polynucleotide, useful for treating disorders
 PT associated with protein truncation, particularly muscular dystrophy, and
 PT related peptides and antibodies.
 XX
 PS Disclosure; Fig 16B; 222pp; English.
 XX
 CC The invention relates to a polynucleotide (I) comprising, or consisting
 CC of, apo-dystrophin-4 inversion sequence appearing as ABK86496, or its
 CC functional equivalents (e.g. the apo-dystrophin-4 cDNA sequence appearing
 CC as ABK86497). Also included are polynucleotides that hybridize to either
 CC strand of (I), a vector containing (I), a cell containing (I) or the
 CC human dystrophin that is expressed on cell surfaces in vivo antibodies
 CC (Ab) specific for the protein and method of screening for leukemia cells
 CC by analysing DNA for presence of (I) or by detecting presence of (II).
 CC The apo-dystrophin-4 inversion sequence is a regulatory element that
 CC controls expression (transcription and translation) of associated DNA,
 CC and may allow read-through of stop codons. The apo-dystrophin-4 inversion
 CC sequence is used in gene therapy of diseases associated with truncation
 CC of proteins, particularly muscular dystrophy and also leukaemia, but more
 CC generally (I) is a regulatory sequence used to control expression of any
 CC attached gene. Analysis of DNA for (I), or detection of proteins (II)
 CC encoded by (I), can be used to screen for leukaemic cells and related
 CC diseases. Antibodies raised against (II) can be used therapeutically, to
 CC inhibit (II) activity, also to detect (II) in screening assays. The
 CC present sequence is a apo-dystrophin-4 cDNA fragment showing the second
 CC direct repeat thought to be responsible for the inversion present in apo-
 CC dystrophin-4
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 0 G; 8 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 621 AAAGAAAG 628
 DB 10 AAAGAAAG 3
 RESULT 226
 ABL9008
 ID ABL99008 standard; cDNA; 10 BP.
 XX
 AC ABL99008;
 XX
 DT 25-JUN-2002 (first entry)
 XX
 DE Mouse neuronal regeneration related SAGE EST 3.
 XX
 KW Mouse; neuronal; regeneration; nerve cell; synaptic efficiency; memory;
 KW learning disorder; serial analysis of gene expression; SAGE;

KW gene expression; hippocampus; expressed sequence tag; EST; ss.
 OS Mus sp.
 XX DE10048893-A1.
 PN 11-APR-2002.
 PD 02-OCT-2000; 2000DE-01048893.
 XX
 PF 02-OCT-2000; 2000DE-01048893.
 XX
 PR (LION-) LION BIOSCIENCE AG.
 PA
 XX WPI; 2002-341428/38.
 DR
 XX New nucleic acids involved in neuronal regeneration, useful in screening
 PT for modulators of regeneration or synaptic efficiency, and potential
 PT therapeutic agents.
 XX
 PS Example 4; Page 8; 38pp; German.
 XX
 CC The invention relates to nucleic acids (ABL98957-ABL99004) involved in
 CC regenerative neuronal processes and encoded proteins (ABB79405-ABB79409)
 CC used to screen for compounds and potential therapeutic agents that
 CC modulate nerve cell regeneration and/or synaptic efficiency. They may
 CC also be used for treatment or diagnosis of defective or pathological
 CC memory and learning conditions. The present sequence is that of an EST
 CC isolated from serial analysis of gene expression (SAGE) experiments
 CC comparing gene expression in the hippocampus of GFAP/L1 transgenic mice
 CC versus a wildtype control. The resultant EST were used to isolate the
 CC nucleic acids of the invention
 XX
 SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 628 GTGCTGGA 635
 DB 1 GTGCTGGA 8
 RESULT 227
 ABK17004/c
 ID ABK17004 standard; DNA; 10 BP.
 XX
 AC ABK17004;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Pyridoxal (Pyridoxine, vitamin B6) Kinase (PDXK) primer #27.
 XX
 KW Pyridoxal kinase; pyridoxine; vitamin B6;
 KW PDXK autoimmune polyglandular disease type 1; transgenic animal;
 KW gene therapy; primer extension; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200190125-A2.
 PD 29-NOV-2001.
 XX
 PF 24-MAY-2001; 2001WO-US016909.
 XX
 PR 24-MAY-2000; 2000US-0206664P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Chew A, Duda A, Koehy B;
 XX WPI; 2002-106169/14.
 DR

XX Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polyNTs, useful
PT for therapeutic purposes, for studying the expression and function of the
PT polyNT, and for expressing pyridoxal protein.
PS
XX Claim 19; Page 14; 135pp; English.
XX
CC The invention describes an isolated human pyridoxal (pyridoxine, vitamin
CC B6) kinase, (PDXK) polynucleotide. The polynucleotide is useful in
CC studying the expression and function of PDXK, and in expressing PDXK
CC protein for use in screening for candidate drugs to treat PDXK related
CC diseases and for therapeutic purposes. A transgenic animal is useful for
CC studying expression of the PDXK isogenes in vivo, for in vivo screening
CC and testing of drugs targeted against PDXK protein, and for testing the
CC efficacy of therapeutic agents and compounds for autoimmune polyglandular
CC disease type 1. The polypeptide is useful for studying the effect of the
CC variation on the biological activity of PDXK and the binding affinity of
CC candidate drugs targeting PDXK for the treatment of autoimmune
CC polyglandular disease type 1. Genotyping and haplotyping is useful for
CC improving the efficacy and reliability of several steps in the discovery
CC and development of drugs for treating diseases associated with PDXK
CC activity, e.g., autoimmune polyglandular disease type 1, to validate PDXK
CC as a candidate agent for treating a specific condition or disease
CC predicted to be associated with PDXK activity, and in the design of
CC clinical trials of candidate drugs. This sequence is one of 38 (see
CC ABK16978-ABK17015) primers used for detecting PDXK gene polymorphisms by
CC primer extension terminates, described in the method of the invention
XX
SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 628 GTGCTGGA 635
DB 9 GTGCTGGA 2
RESULT 228
AAS99195
ID AAS99195 standard; DNA; 10 BP.
XX
AC AAS99195;
DT 12-MAR-2002 (first entry)
XX
XX UDP glycosyltransferase 1 (UGT1A1) allele-specific oligonucleotide #62.
DE
XX UDP glycosyltransferase 1; UGT1A1; human; haplotyping; ss;
KW drug discovery; Gilbert's syndrome; Crigler-Najjar syndrome;
KW allele-specific oligonucleotide.
XX
XX Homo sapiens.
OS
XX WO200179230-A2.
PN
XX 25-OCT-2001.
PD
XX 13-APR-2001; 2001WO-US012273.
PF
XX 18-APR-2000; 2000US-0197514P.
PR
XX (GENA-) GENAISANCE PHARM INC.
PA
XX Chew A, Choi JY, Koshi B, Rounds E;
PI
XX WPI; 2002-075063/10.
DR
XX Genotyping a human UDP glycosyltransferase 1 gene of an individual for
PT determining the haplotype of an individual, involves determining the
PT identity of a nucleotide pair at specific polymorphic sites for two
PT copies of the gene.

XX Claim 18; Page 14; 81pp; English.
PS
XX The invention relates to genotyping a human UDP glycosyltransferase
CC (UGT1A1) gene of an individual, involving determining for the two copies
CC of the UGT1A1 gene present in the individual, the identity of the
CC nucleotide pair at one or more polymorphic sites. The new method is
CC useful for determining whether an individual has a haplotype or haplotype
CC pairs, given in the specification. It is useful for improving the
CC efficacy and reliability of several steps in the discovery and
CC development of drugs for treating diseases associated with UGT1A1
CC activity, e.g., Gilbert's syndrome and Crigler-Najjar syndrome, to
CC validate UGT1A1 as a candidate agent for treating a specific condition or
CC disease predicted to be associated with UGT1A1 activity, and in the
CC design of clinical trials of candidate drugs for treating a specific
CC condition or disease predicted to be associated with UGT1A1 activity. The
CC method is useful to screen for compounds targeting UGT1A1 to treat a
CC specific condition or disease associated with UGT1A1 activity. A nucleic
CC acid (I) comprising a polymorphic variant of a reference sequence for the
CC UGT1A1 gene or cDNA (II) or its fragment is useful in studying the
CC expression and function of UGT1A1, and in expressing UGT1A1 protein for
CC use in screening for candidate drugs to treat diseases related to UGT1A1
CC activity. (I) or (II) is useful for therapeutic purposes. (II) or a
CC recombinant organism comprising (II) is useful for studying expression of
CC the UGT1A1 isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against UGT1A1 protein, and for testing the efficacy of
CC therapeutic agents and compounds for Gilbert's syndrome and Crigler-
CC Najjar syndrome, in a biological system. AAS99134-AAS99203 represent UDP
CC glycosyltransferase 1 gene allele-specific oligonucleotides used in the
CC method of the invention
XX
SQ Sequence 10 BP; 7 A; 0 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 621 AAAGAAAG 628
DB 2 AAAGAAAG 9
RESULT 229
ABV78516/c
ID ABV78516 standard; cDNA; 10 BP.
XX
XX ABV78516;
AC
XX 29-NOV-2002 (first entry)
DT
XX Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:227.
DE
XX SAGE tag; serial analysis of gene expression; human; Th1 cell;
KW activated T cell; T lymphocyte; immune response; expression pattern;
KW preferential expression; immune disorder; EST; expressed sequence tag;
KW ss.
XX
XX Homo sapiens.
OS
XX JP2002186482-A.
PN
XX 02-JUL-2002.
PD
XX 19-DEC-2000; 2000JP-00385816.
PF
XX 19-DEC-2000; 2000JP-00385816.
PR
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA
XX WPI; 2002-594261/64.
DR
XX Human activated Th1 and Th2 cell expression gene group, useful for the
PT diagnosis and treatment of Th1 and Th2-related diseases.
PT

XX PS Claim 19; Page 12; 60pp; Japanese.

XX CC The invention relates to SAGE (serial analysis of gene expression) tags

CC representing groups of genes which are expressed in activated human Th1

CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence

CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif

CC lying nearest to the polyA region of cDNAs derived from a variety of

CC genes. These tags serve to uniquely identify each transcript and can thus

CC be used to analyse the pattern of gene expression in particular cell

CC types. The invention also relates to proteins encoded by the genes

CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and

CC inhibitors of the expression of groups of genes that are expressed in

CC either or both the two cell types. Groups of genes expressed in Th1

CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1

CC and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags

CC representing 171 genes which are more highly expressed in Th1 cells

CC compared with Th2 cells

XX SQ Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 616 CCGGAAAA 623

DB 9 CCGGAAAA 2

RESULT 230

ABV84212

ID ABV84212 standard; cDNA; 10 BP.

AC ABV84212;

XX 12-DEC-2002 (first entry)

DE Human haemoglobin beta-like EST SAGE tag #22.

XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;

KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;

KW expression pattern; differential expression; EST; expressed sequence tag;

XX ss.

XX Homo sapiens.

OS JP2002209591-A.

XX 30-JUL-2002.

XX 19-JAN-2001; 2001JP-00012328.

XX 19-JAN-2001; 2001JP-00012328.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

PA WPI; 2002-631294/68.

XX Human chronic hepatitis C tissue expression exasperating gene group

PT comprises 100 high-ranking genes.

XX Claim 1; Page 10; 139pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags

CC representing groups of genes which are differentially expressed in human

CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced

CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.

CC The SAGE tags of this invention consist of a sequence of 10 nucleotides

CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the

CC polyA region of cDNAs derived from a variety of genes. These tags serve

CC to uniquely identify each transcript and can thus be used to analyse the

CC pattern of gene expression in particular cell types. The invention also

CC relates to proteins encoded by the genes expressed in chronic hepatitis C

CC liver tissue or HCC, antibodies against these proteins, and inhibitors of

CC the expression of groups of genes that are overexpressed in chronic

CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed

CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and

CC treatment of these diseases. Such genes, inhibitors of their expression

CC to uniquely identify each transcript and can thus be used to analyse the

CC pattern of gene expression in particular cell types. The invention also

CC relates to proteins encoded by the genes expressed in chronic hepatitis C

CC liver tissue or HCC, antibodies against these proteins, and inhibitors of

CC the expression of groups of genes that are overexpressed in chronic

CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed

CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and

CC treatment of these diseases. Such genes, inhibitors of their expression

CC or activity, and antibodies against the gene products may be used in the

CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences

CC ABV84191-ABV84290 are SAGE tags representing the 100 most highly

CC expressed genes out of those genes which are overexpressed in chronic

XX hepatitis C liver tissue compared with normal liver tissue

XX SQ Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 622 AAGAAAGT 629

DB 3 AAGAAAGT 10

RESULT 231

ABV84745

ID ABV84745 standard; cDNA; 10 BP.

XX AC ABV84745;

XX 12-DEC-2002 (first entry)

DE Human haemoglobin beta SAGE tag #555.

XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;

KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;

KW expression pattern; differential expression; ss.

XX Homo sapiens.

OS JP2002209591-A.

XX 30-JUL-2002.

XX 19-JAN-2001; 2001JP-00012328.

XX 19-JAN-2001; 2001JP-00012328.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

PA WPI; 2002-631294/68.

XX Human chronic hepatitis C tissue expression exasperating gene group

PT comprises 100 high-ranking genes.

XX Claim 46; Page 26; 139pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags

CC representing groups of genes which are differentially expressed in human

CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced

CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.

CC The SAGE tags of this invention consist of a sequence of 10 nucleotides

CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the

CC polyA region of cDNAs derived from a variety of genes. These tags serve

CC to uniquely identify each transcript and can thus be used to analyse the

CC pattern of gene expression in particular cell types. The invention also

CC relates to proteins encoded by the genes expressed in chronic hepatitis C

CC liver tissue or HCC, antibodies against these proteins, and inhibitors of

CC the expression of groups of genes that are overexpressed in chronic

CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed

CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and

CC treatment of these diseases. Such genes, inhibitors of their expression

CC to uniquely identify each transcript and can thus be used to analyse the

CC pattern of gene expression in particular cell types. The invention also

CC ABV84691-ABV84790 are SAGE tags representing the 100 least highly
CC expressed genes out of those genes which are underexpressed in
CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue
XX
SQ Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 622 AAGAAAGT 629
DB 3 AAGAAAGT 10
|||||

RESULT 232
ID ABK23615/c
ID ABK23615 standard; DNA; 10 BP.

XX AC ABK23615;

XX DT 09-APR-2002 (first entry)

XX DE Transcript tag DNA sequence #204 induced or suppressed by N-myc.

XX KW Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
XX KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;
XX KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.

XX OS Homo sapiens.

XX PN WO200185941-A2.

XX PD 15-NOV-2001.

XX PF 11-MAY-2001; 2001WO-NL000361.

XX PR 11-MAY-2000; 2000EP-00201698.

XX PR 29-JUN-2000; 2000EP-00202284.

XX PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.

XX PI Versteeg R, Caron HN;

XX PS WPI; 2002-066603/09.

XX PT A new nucleic acid library of myc-dependent downstream genes capable of
XX supporting a neoplastic characteristic of cancer is useful to find new
XX therapies and diagnoses for cancer.

XX PS Disclosure; Page 54; 69pp; English.

XX CC The present invention relates to a nucleic acid library comprising myc-
XX dependent downstream genes or their functional fragments essentially
XX capable of supporting a neoplastic character of cancer such as growth,
XX invasion or spread. These myc target or tag sequences are identified by
XX SAGE (serial analysis of gene expression). The library is useful to find
XX new diagnoses and treatments for cancer. The invention is also useful to
XX enhance production of recombinant proteins in a production system with
XX high expression of endogenous or transfected myc oncogenes. ABK23412-
XX ABK23828 represent transcript tag DNA sequences that are activated or
XX repressed by N-myc in human neuroblastoma

XX SQ Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 621 AAGAAAG 628
DB 8 AAGAAAG 1
|||||

RESULT 233
ID ABK28549
ID ABK28549 standard; DNA; 10 BP.

XX AC ABK28549;

XX DT 09-APR-2002 (first entry)

XX DE Paraoxonase 2 (PON2), primer extension oligonucleotide #22.

XX KW Paraoxonase 2; PON2; coronary heart disease;
XX KW primer extension oligonucleotide; primer; ss.

XX OS Homo sapiens.

XX PN WO200188202-A1.

XX PD 22-NOV-2001.

XX PF 18-MAY-2001; 2001WO-US016352.

XX PR 18-MAY-2000; 2000US-0205145P.

XX PA (GENA-) GENAISANCE PHARM INC.

XX PI Anastasio AE, Chew A, Choi JY, Denton RR, Lee HH, Nandabalan K;

XX PS WPI; 2002-121985/16.

XX PT An isolated polynucleotide comprising a paraoxonase 2 (PON2) isogene
XX encodes a pharmaceutically important protein for the identification of
XX polymorphisms at the PON2 locus.

XX PS Claim 19; Page 14; 125pp; English.

XX CC The invention describes an isolated polynucleotide sequence comprising a
XX paraoxonase 2 (PON2) isogene. Primers and probes allow identification of
XX this sequence and its polymorphisms and are useful for identifying which
XX isoform of paraoxonase 2 a person carries. Identification of a PON2
XX isoform allows tailored pharmaceutical treatment to be designed and
XX administered. PON2 is a particularly important gene for the treatment of
XX coronary heart disease. This sequence represents a primer extension
XX oligonucleotide used for detecting PON2 gene polymorphisms, described in
XX the method of the invention

XX SQ Sequence 10 BP; 6 A; 0 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 618 GGAAAAGA 625

DB 3 GGAAAAGA 10
|||||

RESULT 234

ID ABK81797/c

XX ID ABK81797 standard; DNA; 10 BP.

XX AC ABK81797;

XX DT 13-AUG-2002 (first entry)

XX DE Human CHRM5 gene polymorphism detection oligonucleotide primer #3.

XX KW Human; cholinergic receptor muscarinic 5; CHRM5; genotyping; haplotyping;

XX KW single nucleotide polymorphism; SNP; primer; ss.

XX OS Homo sapiens.

XX PN WO200232924-A2.

XX 25-APR-2002.
 PD 11-OCT-2001; 2001WO-US032022.
 PF 19-OCT-2000; 2000WO-US029071.
 PR (GENA-) GENAISSANCE PHARM INC.
 XX Bieglecki KM, Chew A, Choi JY, Denton RR, Nandabalan K;
 PI Sausker EA, Stephens JC;
 PI WPI; 2002-435523/46.
 DR Novel cholinergic receptor, muscarinic 5 polynucleotide useful
 XX therapeutically and in screening for candidate drug to treat diseases
 PT related to the receptor activity.
 PT Claim 16; Page 14; 72pp; English.
 PS The present invention relates to a new cholinergic receptor, muscarinic 5
 XX (CHRM5) polynucleotide comprising a sequence which is a polymorphic
 CC variant for a reference sequence for the CHRM5 gene or its fragment, or a
 CC polymorphic variant of a reference sequence for a CHRM5 cDNA or its
 CC fragment. The invention is useful in drug screening assays. The molecules
 CC of the invention are useful in studying the expression and function of
 CC CHRM5, and in expressing CHRM5 protein for use in screening for candidate
 CC drugs to treat diseases related to CHRM5 activity. The methods of the
 CC invention are useful in developing diagnostic tests and therapeutic
 CC treatments. The method is also useful in the design of clinical trials of
 CC candidate drugs for treating specific condition or disease associated
 CC with CHRM5 activity and is useful in determining whether an individual
 CC has one of the haplotypes or one of the haplotype pairs. The invention is
 CC useful in a variety of diagnostic and prognostic formats and therapeutic
 CC methods. The invention is also useful in genotyping and/or haplotyping
 CC the CHRM5 gene in an individual. The present nucleic acid sequence
 CC represents one of a collection of oligonucleotide primers (ABK81795-
 CC ABK81814) that were used in the invention to detect polymorphisms in the
 CC human CHRM5 gene
 XX
 SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 627 AGTGCTGG 634
 DB |||||
 10 AGTGCTGG 3
 RESULT 235
 AAL39786
 ID AAL39786 standard; DNA; 10 BP.
 XX
 AC AAL39786;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE SMOH polymorphism detecting primer SEQ ID No 101.
 XX
 KW Cytostatic; polymorphic variant; single nucleotide polymorphism; SMOH;
 KW human smoothened Drosophila homologue; basal cell carcinoma; BCC;
 KW gene therapy; antisense gene therapy; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200229004-A2.
 XX
 XX 11-APR-2002.
 PD 04-OCT-2001; 2001WO-US031304.
 PF
 XX

PR 04-OCT-2000; 2000US-0237871P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Bentivegna SC, Choi JY, Koshy B, Lee HH, Sausker EA;
 PI WPI; 2002-519113/55.
 DR New genetic variants of smoothened Drosophila homolog (SMOH) gene useful
 XX for therapeutic purposes and for expressing SMOH protein useful in
 PT identifying drugs to treat basal cell carcinomas.
 PT Claim 17; Page 15; 179pp; English.
 PS The invention relates to an isolated polynucleotide comprising a sequence
 XX which is a polymorphic variant of a reference sequence for the human
 CC smoothened Drosophila homologue (SMOH) gene or its fragment, or a
 CC polymorphic variant of a reference sequence for a SMOH cDNA or its
 CC fragment. A new isolated polypeptide is useful for screening for drugs
 CC targeting the polypeptide. A new method is useful for identifying an
 CC association between a trait such as a clinical response to a drug
 CC targeting SMOH and a haplotype or haplotype pair of SMOH gene. The
 CC methods have applicability in developing diagnostic tests and therapeutic
 CC treatments for basal cell carcinomas (BCCs). The isolated polynucleotide
 CC is useful for studying the expression and function of SMOH and expressing
 CC SMOH protein for use in screening for candidate drugs to treat diseases
 CC related to SMOH activity. The polymorphism and haplotype data are useful
 CC for validating whether SMOH is a suitable target for drugs to treat BCCs,
 CC screening for the drugs and reducing bias in clinical trials of the
 CC drugs. The isolated polynucleotide is useful for therapeutic purposes.
 CC The new method, an oligonucleotide and kit of the invention are useful
 CC for determining whether an individual has one of the haplotypes or the
 CC haplotype pairs. The polynucleotides of the invention can be used to
 CC treat disorders by gene therapy and antisense gene therapy. This
 CC polynucleotide sequence represents a primer used for detecting human
 CC smoothened Drosophila homologue gene polymorphisms of the invention
 XX
 SQ Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 618 GGAAAAAGA 625
 DB |||||
 1 GGAAAAAGA 8
 RESULT 236
 ABX79755/c
 ID ABX79755 standard; cDNA; 10 BP.
 XX
 AC ABX79755;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE EST polymorphic DNA repeat polynucleotide #80.
 XX
 KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Friedreich's ataxia; myotonic dystrophy; hyperandrogenemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
 XX
 OS Homo sapiens.
 XX
 PN US6472154-B1.
 XX
 XX 29-OCT-2002.
 PD 31-DEC-1999; 99US-00475947.
 PF
 XX

PR 31-DEC-1999; 99US-00475947.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Garner HR, Wren JD, Minna JD, Fondon JW;
 XX WPI; 2003-208818/20.
 XX
 XX Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.
 XX
 XX Example; Col 299; 588pp; English.
 XX
 XX The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 0 G; 7 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 621 AAAGAAAG 628
 Db | | | | | | | |
 9 AAAGAAAG 2
 RESULT 237
 ABX79817
 ID ABX79817 standard; cDNA; 10 BP.
 XX
 AC ABX79817;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE EST polymorphic DNA repeat polynucleotide #142.
 XX
 KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW Polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Friedreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
 XX
 OS Homo sapiens.
 XX
 FN US6472154-B1.
 XX
 PD 29-OCT-2002.
 XX
 PF 31-DEC-1999; 99US-00475947.
 XX
 PR 31-DEC-1999; 99US-00475947.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Garner HR, Wren JD, Minna JD, Fondon JW;
 XX

DR WPI; 2003-208818/20.
 XX
 XX Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.
 XX
 XX Example; Col 667; 588pp; English.
 XX
 XX The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs
 XX
 SQ Sequence 10 BP; 7 A; 0 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 621 AAAGAAAG 628
 Db | | | | | | | |
 3 AAAGAAAG 10
 RESULT 238
 ACA94606
 ID ACA94606 standard; DNA; 10 BP.
 XX
 AC ACA94606;
 XX
 DT 18-JUL-2003 (first entry)
 XX
 DE DNA tag from human transcript repressed in adenomas/cancers #139.
 XX
 KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
 KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
 KW kidney proximal tubule.
 XX
 OS Homo sapiens.
 XX
 FN WO2003022863-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 09-SEP-2002; 2002WO-US028518.
 XX
 PR 07-SEP-2001; 2001US-0317494P.
 PR 30-MAY-2002; 2002US-0383805P.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Buckhaults P, Kinzler KW, Vogelstein B;
 XX
 XX WPI; 2003-313220/30.
 XX
 XX Detecting colorectal cancer in a subject, involves detecting macrophage
 PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
 PT of the subject.
 XX
 XX Disclosure; Page 30; 59pp; English.
 XX

CC The invention relates to detecting CC (colorectal cancer e.g. colorectal
 CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
 CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
 CC amount of MIC or RDP detected to that in normal subjects, where an
 CC elevated amount of MIC or RDP in the subject is an indicator of CC in
 CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
 CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
 CC mRNA detected to that in normal subjects, where an elevated amount of MIC
 CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
 CC isolating epithelial cells from blood of a subject, isolating an mRNA
 CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
 CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
 CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
 CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
 CC of CC in the subject; (d) contacting blood or faeces of a subject, with
 CC an RDP substrate, detecting activity of RDP in the blood or faeces by
 CC detection of increased reaction product or decreased RDP substrate, and
 CC comparing the amount of activity of RDP in blood or faeces of the subject
 CC to that in normal subjects, where an elevated amount of activity of RDP
 CC in the blood or faeces of the subject is an indicator of CC in the
 CC subject; (e) administering to a subject an antibody which specifically
 CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
 CC labeled with a moiety which is detectable from outside of the subject and
 CC detecting the moiety in the subject from outside of the subject, where an
 CC area of localisation of the moiety within the subject but outside the
 CC proximal tubules of the kidney identifies CC; or (f) administering to a
 CC subject a substrate for RDP, the substrate being labeled with a
 CC detectable moiety, isolating faeces or blood from the subject, and
 CC detecting in the faeces or blood RDP reaction product or RDP substrate
 CC with the detectable moiety, where increased product or decreased
 CC substrate in the faeces or blood indicates CC in the subject. The methods
 CC are useful for detecting colorectal cancer in a subject. The present
 CC sequence is a DNA tag derived from a human transcript whose expression is
 CC repressed in colorectal cancer or colorectal adenoma
 XX
 SQ Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 622 AAGAAAGT 629
 |||||
 Db 3 AAGAAAGT 10

RESULT 239
 ACC41703
 ID ACC41703 standard; DNA; 10 BP.
 XX
 AC ACC41703;
 XX
 DT 21-MAY-2003 (first entry)

XX Zinc finger protein DNA-binding domain target sequence SEQ ID NO:250.
 DE Zinc finger domain; zinc finger; zinc finger binding domain; probe;
 KW chimeric nucleic acid; library; PCR primer; ss.
 XX Synthetic.
 OS
 XX WO2003016571-A1.
 PN Petersen N, Rounds E, Sausker EA, Tirrell C;
 PD 27-FEB-2003.

XX 17-AUG-2002; 2002WO-KR001560.
 PF
 XX 17-AUG-2001; 2001US-0313402P.
 PR
 XX 22-APR-2002; 2002US-0374355P.
 PR
 PA (TOOL-) TOOLGEN INC.

XX Kim J, Bae K, Park K, Kwon Y, Ryu E, Hwang M;
 PI

XX
 DR
 XX
 PT
 PT
 XX
 PS
 XX

WPI; 2003-268344/26.

New library comprising polypeptides having zinc finger domains, useful
 for producing chimeric nucleic acids.

Claim 40; Page 104; 234pp; English.

CC The present invention describes a library comprising polypeptides. Each
 CC polypeptide comprises a first or second zinc finger domain. The domains
 CC of each polypeptide are identical to a zinc finger domain from a
 CC naturally occurring protein and either do not occur in the same naturally
 CC occurring protein or occur in the same naturally occurring protein in a
 CC different configuration than in the polypeptide. The domains vary among
 CC polypeptides. Also described: (1) producing chimeric nucleic acids; (2)
 CC generating an artificial zinc finger polypeptide that specifically binds
 CC to a target DNA site; and (3) identifying a nucleic acid encoding a zinc
 CC finger polypeptide that specifically recognises a target DNA site. The
 CC library can be used for producing chimeric nucleic acids. ACC41551 to
 CC ACC41738 and ABR40919 to ABR41015 represent nucleotide and amino acid
 CC sequences given in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 9 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 620 AAAAGAAA 627
 |||||
 Db 1 AAAAGAAA 8

RESULT 240
 ADG98554/c
 ID ADG98554 standard; DNA; 10 BP.
 XX
 AC ADG98554;
 XX
 DT 11-MAR-2004 (first entry)

XX Human CETP gene allele specific extension PCR primer #15.
 DE
 XX human; cholesteryl ester transfer protein; CETP;
 KW single nucleotide polymorphism; SNP; drug screening; atherosclerosis;
 KW cardiovascular disease; hypercholesterolaemia;
 KW allele specific oligonucleotide; ss; extension PCR; primer.
 XX Homo sapiens.
 OS
 XX WO2003091277-A2.
 PN
 PD 06-NOV-2003.
 XX 28-APR-2003; 2003WO-US013288.
 PF
 XX 26-APR-2002; 2002US-0375791P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.

XX Anastasio AE, Chew A, Kazemi A, Lachowicz M, Lee HH, Parks KE;
 PI Petersen N, Rounds E, Sausker EA, Tirrell C;
 XX WPI; 2003-865576/80.
 DR
 XX New isolated polynucleotide useful for haplotyping and/or genotyping
 PT cholesteryl ester transfer protein (CETP) gene in an individual or in
 PT screening for drugs useful in treating diseases associated with CETP
 PT activity.
 XX
 PS Claim 45; SEQ ID NO 186; 250pp; English.
 XX The invention comprises the amino acid and coding sequences of the human

CC cholesterol ester transfer protein (CETP), the invention also comprises
 CC polymorphisms identified within the CETP gene. The DNA and protein
 CC sequences of the invention are useful in haplotyping and/or genotyping
 CC the CETP gene in an individual. The DNA and protein sequences may also be
 CC used to screen drugs or compounds targeting the CETP or its variant to
 CC treat a condition or disease associated with CETP (e.g. atherosclerosis,
 CC cardiovascular disease or hypercholesterolaemia). The present DNA
 CC sequence represents an allele specific extension PCR primer for the human
 CC CETP gene.

XX Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 626 AAGTGCTG 633
 |||||
 Db 8 AAGTGCTG 1

RESULT 241
 ADH78855/C
 ID ADH78855 standard; DNA; 10 BP.

XX AC ADH78855;

DT 22-APR-2004 (first entry)

DE Human apical iodide transporter 3' intron extremity SEQ ID NO:43.
 DE ds; human; apical iodide transporter; cytostatic; antithyroid;
 KW gene therapy; hypersecretion of thyroid hormone; thyroid tumour;
 KW radioactive iodine; iron.

XX OS Homo sapiens.

XX PN FR2837492-A1.

PD 26-SEP-2003.

XX PF 21-MAR-2002; 2002FR-00003572.

XX PR 21-MAR-2002; 2002FR-00003572.

XX PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

XX PI Leblanc G, Pourcher T;

XX WPI; 2003-790461/75.

XX New human apical iodide transporter useful for screening of compounds
 PT able to modulate apical iodide transport in cells for treatment,
 PT prevention or diagnosis of dysfunctional iodide transport.

XX Disclosure; SEQ ID NO 43; 46pp; French.

XX The invention relates to a novel isolated, purified protein related to a
 CC apical iodide transporter protein. A protein of the invention has
 CC cytotatic, and antithyroid activity. A protein of the invention is used
 CC for screening of compounds able to modulate apical iodide transport in
 CC cells. The nucleic acid encoding the protein can be used for production
 CC of recombinant protein or to generate transgenic animals, useful in
 CC screening for agents that modulate activity of the protein. The protein,
 CC its peptides, nucleic acids encoding it, vectors containing the nucleic
 CC acids and antibodies against the protein, are useful for prevention,
 CC treatment (including gene therapy) of diseases that involve dysfunction
 CC of apical iodide transport, e.g. hypersecretion of thyroid hormone or
 CC development of thyroid tumours. The protein can also be used to counter
 CC accumulation of, or contamination by, radioactive iodine, and its peptide
 CC fragments are used to raise antibodies. The present sequence is used in
 CC the exemplification of the invention.

XX

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